GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 18:25:29 ; Search time 23795.2 seconds
       (without alignments)
       1132.312 Million cell updates/sec

Title: US-09-227-881-3
Perfect score: 6169
Sequence: 1 atctttgttcagttacctc.........cttgtgccctccatgtcag 6169
Scoring table: IDENTITY_NUC
       Gapop 10.0 , Gapext 1.0
Searched: 1033670 seqs, 218378903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
       Maximum Match 100%
       Listing first 45 summaries

Database :   GenEmbl:*

1:	gb_ba1:*
2:	gb_ba2:*
3:	gb_om:*
4:	gb_ov:*
5:	gb_pat:*
6:	gb_ph:*
7:	gb_pl1:*
8:	gb_pl2:*
9:	gb_pr1:*
10:	gb_pr2:*
11:	gb_pr3:*
12:	gb_ro:*
13:	gb_sy:*
14:	gb_un:*
15:	em_fun:*
16:	em_hum1:*
17:	em_hum2:*
18:	em_ln:*
19:	em_om:*
20:	em_or:*
21:	em_ov:*
22:	em_pat:*
23:	em_ph:*
24:	em_pl:*
25:	em_ro:*
26:	em_sts:*
27:	em_sy:*
28:	em_un:*
29:	em_vi:*
30:	gb_ba3:*
31:	gb_in1:*
32:	gb_in2:*
33:	gb_in3:*
34:	gb_pl3:*
35:	gb_pr4:*
36:	em_ba1:*
37:	em_ba2:*
38:	em_htg1:*
39:	em_htg2:*
40:	em_htg3:*
41:	em_htg4:*
42:	em_htg5:*
43:	em_htg6:*
44:	em_htg7:*
45:	em_htg8:*
46:	em_htg9:*
47:	em_htg10:*
48:	em_htg11:*
49:	em_htg12:*
50:	em_htg13:*
51:	em_htg14:*
52:	em_htg15:*
53:	em_htg16:*
54:	em_htg17:*
55:	em_htg18:*
56:	em_htg19:*
57:	em_htg20:*
58:	em_htg21:*
59:	em_htg22:*
60:	em_htg23:*
61:	em_hum3:*
62:	em_hum4:*
63:	em_hum5:*
64:	em_hum6:*
65:	gb_pr5:*
66:	gb_pr6:*
67:	gb_pr7:*
68:	gb_htg1:*
69:	gb_htg2:*
70:	gb_htg3:*
71:	gb_htg4:*
72:	gb_htg5:*
73:	gb_htg6:*
74:	gb_htg7:*
75:	gb_htg8:*
76:	gb_htg9:*
77:	gb_htg10:*
78:	gb_htg11:*
79:	gb_htg12:*
80:	gb_htg13:*
81:	gb_htg14:*
82:	gb_htg15:*
83:	gb_htg16:*
84:	gb_htg17:*
85:	gb_htg18:*
86:	gb_htg19:*
87:	gb_htg20:*
88:	gb_htg21:*
89:	gb_htg22:*
90:	gb_htg23:*
91:	gb_sts1:*
92:	gb_sts2:*
93:	gb_vi1:*
94:	gb_vi2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
c 1	6105.4	99.0	79376	65	Z98750 Human DNA s
2	6054.4	98.1	170425	77	AC024490 Homo sapi
3	5300	85.9	5300	11	AF007562 Homo sapi
4	2677.4	43.4	2800	66	HSMYOC1 Homo sapi
5	1190.4	19.3	1228	9	AB006865 Homo sapi
6	1084.4	17.6	1086	56	AB006865S1 Homo sapi
7	651.2	10.6	1934	35	Z97171 Homo sapien
8	640.4	10.4	1999	5	D88214 Homo sapien
9	640.4	10.4	1999	5	AR030962 Homo sapien
10	640.4	10.4	1999	5	AR066022 Sequence
11	640.4	10.4	2000	5	AR069089 Sequence
12	640.4	10.4	2002	5	A84847 Sequence 2

RESULT 1

	#					accession		description
	13	635.6	10.3	2000	5	A84850	A84850	Sequence 2
	14	626.4	10.2	2051	66	HSAF001620	AF001620	Homo sapi
	15	604.4	9.8	1512	5	A84848	A84848	Sequence 3
	16	604.4	9.8	1512	5	AR030963	AR030963	Sequence
	17	604.4	9.8	1512	5	AR066023	AR066023	Sequence
	18	604.4	9.8	1512	5	AR069090	AR069090	Sequence
	19	599.6	9.7	1512	5	A84851	A84851	Sequence 3
	20	585.0	9.5	2800	12	MMTSMYOC1	MMTSMYOC1	Sequence
	21	559	9.1	1016	12	MMTMIGP1	AF041333	Mus muscu
	22	556.6	9.0	1969	5	AR020502	AR020502	Sequence 2
	23	556.6	9.0	1969	5	I36470	I36470	Sequence 2
	24	519.6	8.4	1491	5	AR020503	AR020503	Sequence 2
	25	519.6	8.4	1491	5	I36471	I36471	Sequence 3
	26	440.8	7.1	2004	12	AB013592	AB013592	Mus muscu
	27	440.8	7.1	2059	12	AF039869	AF039869	Mus muscu
	28	440.8	7.0	2044	12	AB019393	AB019393	Rattus no
	29	426.2	6.9	2058	12	AF093567	AF093567	Rattus no
	30	398.8	6.5	1473	3	AB027758	AB027758	Bos tauru
	31	217	3.5	228	11	AF007564	AF007564	Homo sapi
o	32	189.8	3.1	161577	10	AC007688	AC007688	Homo sapi
o	33	189.8	3.1	193123	77	AC023790	AC023790	Homo sapi
o	34	189	3.1	199722	71	AC012404	AC012404	Homo sapi
o	35	187.8	3.0	97037	9	AC004973	AC004973	Homo sapi
o	36	187.8	3.0	135038	67	HUMWXD7703	L78810	Homo sapien
o	37	185.8	3.0	76727	65	HS821D11	AL021453	Human DNA
o	38	185.8	3.0	152044	79	AC026395	AC026395	Homo sapi
o	39	185.8	3.0	157057	78	AC025947	AC025947	Homo sapi
o	40	185.8	3.0	161699	72	AC015488	AC015488	Homo sapi
o	41	185.8	3.0	184656	86	AL161726	AL161726	Homo sapi
c	42	185.8	3.0	200681	69	AC008755	AC008755	Homo sapi
c	43	185.8	3.0	201372	86	AL157941	AL157941	Homo sapi
c	44	184.8	3.0	146100	89	AP001813	AP001813	Homo sapi
c	45	184.8	3.0	163494	89	AP002391	AP002391	Homo sapi

ALIGNMENTS

LOCUS   HS454G6   79376 bp   DNA   PRI   23-NOV-1999
DEFINITION Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains
            trabecular meshwork inducible glucocorticoid response protein,
            TIGR, myocilin, ESTs and STS.
ACCESSION   Z98750
VERSION   Z98750.1 GI:2887277
KEYWORDS   1q24; myocilin; TIGR.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 79376)
  AUTHORS   Deadman,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (27-OCT-1997) Chromosome 1 Project Group
            (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquires:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT   This sequence has been finished according to sequence map criteria
            as follows. An attempt is made to resolve all sequencing problems,
            such as compressions and repeats, but not necessarily within known
            annotated human repeat sequence elements (e.g. Alu). Where the
            sequence is ambiguous, there is an annotation using the 'unsure'
            feature key.
            The true left end of clone 454G6 is at 1 in this sequence. The true
            left end of clone 560B9 is at 79273.
            454G6 is from the library RPCI3 constructed at the Roswell Park
            Cancer Institute by the group of Pieter de Jong.
            For further details see http://bacpac.med.buffalo.edu/.
            On Feb 14, 1998 this sequence version replaced gi:2465060.
            IMPORTANT: This sequence is not the entire insert of clone 454G6.
            It may be shorter because we have only sequence overlapping sections
            once, or longer because we arrange for a small overlap between
            neighbouring submissions.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variations annotated may not be found in the sequence submission
            corresponding to the overlapping clone as we submit sequences with
            only a small overlap as described above.
            This sequence was generated from part of bacterial clone contigs of
            human chromosome 1, constructed by the Sanger Centre chromosome 1
            mapping group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1/

FEATURES   Location/Qualifiers
     source   1..79376
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q24"
                     /clone="RP3-454G6"
                     /clone_lib="RPCI-3"
     prim_transcript 1914..>3968
                     /note="match: multiple ESTs
                     match: R56676 AA043968 W63639 F120081 AA046699
                     match: F02925 AA131540 W00634 R36066 AA313383
                     match: AA163561 F02925 AA131540 W00534 R36066
                     match: AA313383 AA163561 N89173 AA174814 AA057059
                     match: AA329084 W47082 AA043955 AA341783 AA355681
                     match: AA046487 AA369741 H08313 AA186895 H32730
                     match: H08333 H08236 N42052 D61944 R27102 N32353
                     match: N30491 AA307150 AA192"
     repeat_region   435..472
                     /note="19 copies of 2 mer 82 % conserved"
     repeat_region   3703..3746
                     /note="22 copies of 2 mer 89 % conserved"
     repeat_region   4051..4183
                     /note="AluSq repeat: matches 1..133 of consensus
                     incomplete repeat."
     repeat_region   4200..4502
                     /note="AluSq repeat: matches 2..301 of consensus"
     repeat_region   4659..4851
                     /note="AluSx repeat: matches 2..194 of consensus
                     incomplete repeat."
     repeat_region   5216..5345
                     /note="AluJo repeat: matches 132..1 of consensus
                     incomplete repeat."
     repeat_region   7759..7907
                     /note="MIR repeat: matches 174..1 of consensus "
     repeat_region   7933..9328
                     /note="TIGGER1 repeat: matches 1..1472 of consensus"
     repeat_region   9332..9626
                     /note="AluSg repeat: matches 1..289 of consensus"
     repeat_region   9639..10335
                     /note="TIGGER1 repeat: matches 1..2174 of consensus"
     repeat_region   10343..10642
                     /note="AluSp repeat: matches 1..300 of consensus"
     repeat_region   10643..10856
                     /note="TIGGER1 repeat: matches 1469..2417 of consensus"
     misc_feature   <10903..>16855
                     /note="endogenous retroviral sequence"
     repeat_region   10949..11384
                     /note="LTR2 repeat: matches 31..449 of consensus"
     repeat_region   15835..15870
                     /note="18 copies of 2 mer 83 % conserved"
     repeat_region   16856..17286
                     /note="LTR2 repeat: matches 31..449 of consensus"
     repeat_region   17287..17574
                     /note="LTR2 repeat: matches 15..300 of consensus"
     repeat_region   18294..18877
                     /note="THE1B repeat: matches 358..1 of consensus"
     repeat_region   19180..19767
                     /note="AluY repeat: matches 301..2 of consensus"
     repeat_region   19767..20013
                     /note="MLT2_internal repeat: matches 5002..4750 of
                     consensus"

```
repeat_region    20051..20118
                 /note="MLT1F repeat: matches 539..471 of consensus"
repeat_region    20130..20261
                 /note="AluYb repeat: matches 131..1 of consensus
                 incomplete repeat"
repeat_region    20264..20722
                 /note="MLT1F repeat: matches 482..1 of consensus"
repeat_region    20858..21223
                 /note="MSTD repeat: matches 394..1 of consensus"
repeat_region    21216..21302
                 /note="MLT2A_internal repeat: matches 4520..4433 of
                 consensus"
repeat_region    21403..21703
                 /note="MLT2A_internal repeat: matches 3887..3580 of
                 consensus"
repeat_region    21978..22357
                 /note="MLT2A_internal repeat: matches 3218..2839 of
                 consensus"
repeat_region    22363..22524
                 /note="MLT2A_internal repeat: matches 2495..2317 of
                 consensus"
repeat_region    22531..22839
                 /note="AluSx repeat: matches 302..1 of consensus"
repeat_region    23007..23309
                 /note="AluJo repeat: matches 298..6 of consensus"
misc_feature     23286..>23680
                 /note="AluSp repeat: matches 3..301 of consensus"
misc_feature     complement(23655..24072)
                 /note="STS G07544"
repeat_region    24008..24290
                 /note="AluJo repeat: matches 298..6 of consensus"
repeat_region    25895..26364
                 /note="LTR2 repeat: matches 2..449 of consensus"
repeat_region    26397..26697
                 /note="AluSq repeat: matches 1..302 of consensus"
repeat_region    26719..27021
                 /note="AluSx repeat: matches 1..302 of consensus"
repeat_region    29037..29934
                 /note="AluSx repeat: matches 300..3 of consensus"
repeat_region    30028..30310
                 /note="AluSx repeat: matches 1..301 of consensus"
repeat_region    30402..30615
                 /note="MLT2B repeat: matches 264..404 of consensus"
repeat_region    30402..30559
                 /note="AluSx repeat: matches 1..301 of consensus"
prim_transcript  <30801..>31136
                 /note="match: 5' EST AA256902 clone 682136"
repeat_region    30980..31222
                 /note="MLT2A repeat: matches 264..453 of consensus"
repeat_region    31232..31528
                 /note="MER4B repeat: matches 199..431 of consensus"
repeat_region    31530..31654
                 /note="AluSc repeat: matches 299..1 of consensus"
repeat_region    31836..32135
                 /note="MER4B repeat: matches 417..540 of consensus"
repeat_region    33200..33201
                 /note="AluY repeat: matches 300..1 of consensus"
repeat_region    33365..33493
                 /note="AluJo repeat: matches 186..287 of consensus
                 incomplete repeat"
repeat_region    33283..33399
                 /note="MIR repeat: matches 206..67 of consensus"
repeat_region    33408..33667
                 /note="MIR repeat: matches 77..196 of consensus"
repeat_region    33956..34043
                 /note="AluY repeat: matches 1..291 of consensus"
repeat_region    34725..34904
                 /note="MIR repeat: matches 80..167 of consensus"
repeat_region    34907..35507
                 /note="AluJo repeat: matches 299..127 of consensus
                 incomplete repeat"
repeat_region    35212..35344
                 /note="AluY repeat: matches 300..1 of consensus"
                 /note="AluJb repeat: matches 133..1 of consensus
                 incomplete repeat"
repeat_region    35545..36842
                 /note="AluJo repeat: matches 299..1 of consensus"
repeat_region    38190..38379
                 /note="MER3 repeat: matches 209..13 of consensus"
repeat_region    38382..38682
                 /note="AluSx repeat: matches 1..302 of consensus"
repeat_region    38836..38968
                 /note="MIR2 repeat: matches 145..2 of consensus"
repeat_region    38983..39279
                 /note="AluJb repeat: matches 3..296 of consensus"
repeat_region    39418..39773
                 /note="THE1A repeat: matches 354..2 of consensus"
repeat_region    39775..40120
                 /note="THE1B-INTERNAL repeat: matches 1580..1234 of
                 consensus"
repeat_region    40757..41023
                 /note="AluJo repeat: matches 37..301 of consensus
                 incomplete repeat"
repeat_region    41307..41589
                 /note="AluSq repeat: matches 21..303 of consensus

Query Match
Best Local Similarity  99.0%;   Score 6105.4;   DB 65;   Length 79376;
Matches 6165;  Conservative  99.8%;  Pred. No. 0;  Mismatches 0;  Indels 9;  Gaps 5;

Qy        1 atctttgttcagtttacctccagggctattatgaaatgaaatgaggataaccaatgtgaaag        60
            ||||||||||||||||||||| ||||||||||||||||| |||| ||| |||||||||||||
Db    68406 ATCTTTGTTCAGTTTACCTTCAGGGCTATTATGAAATGAGAATGAGAATAACCAATGTGAAAG    68347

Qy       61 tcctataaactgtatagcctccattcgtgatgtatgtcttgtcaggtgagatgaagaatca       120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68346 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTGTCAGGATGAGATAAAGAAATCA    68287

Qy      121 ggaagaaggagtatccacgttagccaagtgtccaggtctgtctcgtcttatttagtga       180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68286 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGGCTGTTCAGGTCTTGCTCTTATTTAGTGA    68227

Qy      181 cagatgttgctcctgacagaagctattctccaggaaacatcacatccaatatggtaaatc       240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68226 CAGATGTTGCTCCTGACACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC    68167

Qy      241 catcaaaacaggagctaaaacaaacacgggaatgatgagagcacctgcccaaggaaaatg       300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68166 CATCAAAACAGGAGCTAAGAAAACAGGAATGATGAGAGCACTTGCCCAAGGAAAAATGCCAG    68107

Qy      301 gagagcaaaataatgatgaaaaataaacttttcccttgtcttttaatttcaggaaaaaatg       360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68106 GAGAGCAAATAATAATGATGAAAAATAAACTTTTCCCTTGTTTTTAATTTCAGGAAAAAATG    68047

Qy      361 atgaggagccaaaatcaatgaataggaaacagctcagaagaaaagagtgttctccaaattgg       420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68046 ATGAGGAGCCAAAAATCAATGAATAGGAAAACAGCTCAGAAAAAAAGAGATGTTTCCAAATTGG    67987

Qy      421 taattaagtatattttgttcctttggaagagagacctccaatgtgagctgatgggaaaatggga       480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    67986 TAATTAAGTATATTTTGTTCCTTTGGAAGAGAGACCTCCAATGTGAGCTTGATGGGAAAATGGGAA    67927

Qy      481 aaacgtcaaaagcatgatccgatcagatcccaaagtgattattattttaaaaaaccagat       540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    67926 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGATTATTTTATTTTAAAAAACCAGAT    67867

Qy      541 ggcatcacctctggggaggcaagtcaggaaggtcatgttagcaaggacataacaataac       600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    67866 GGCATCACCTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC    67807

Qy      601 agcaaaatcaaaatccgcaaaatcccgaggaggaagaaatgtggggaagcttcataac       660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    67806 AGCAAAAATCAAAATCCGCAAAATGCAGAAGAGGAAGAAAATGGGACTGGGGAAAGCTTCATATAC    67747

Qy      661 agtggattaggcagttgaccatgttcgcaacacctccgtcctataccagggaaccacaaa       720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    67746 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAAACACAAAA    67687
```

```
Qy    721 attgactgggctaagcctggactttcaagggaaatatgaaaaactgagagcaaaacaaaa  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67686 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 67627

Qy    781 gacatggttaaagggcaaccaacacttgtgagccttcaagcagcagtgccctcagca     840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67626 GACATGGTTAAAAGGCAACCAACAATTGTGAGCCTTCAAAGCAGCAGTGCCCTCAGCA   67567

Qy    841 gggaaccctgaggcatttgcctttaggaaggaagcccagttttctttaaagaaactc    900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67566 GGGACCCTGAGGCCATTTGCCTTTAGGAAGGCCCAGTTTTCTTTAAGGAATCTTAAGAAACTC 67507

Qy    901 ttcgaaagtacatgaacgtttaaccatttaaacatttcaggatataaaacaaatatg     960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67506 TTTAGAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCCGATGGCAAT   67447

Qy    961 tttagacatgggtcccaattttatataaagtcaggcatacaaggataacgtgtcccagctcc 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67446 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 67387

Qy   1021 ggatagtcagaaatcatcaggccccgatcgtgtctgtcccaccacctcactgttttca  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67386 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGGAATGATC 67327

Qy   1081 tgtcaatagccctcacacacacaggcccgatcgtgtctgtcctacacactgtatctgtctac 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67326 TGTCATAGCCCTCACACACACAGGCCCGATGTGTGTCTGTCCTACACACTGTATGCTCTAC 67267

Qy   1141 gtgtgcctcaactgttaacgtcatctccagttaggtccattacaagtgtctccagctcc 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67266 GTGGCCTCAACCATTGTTAACGTCATCTCCAGTTACAAATGCCAACTCCC 67207

Qy   1201 tgtggctagctgggactacagggtctccccactctctagacttctccatcacgatgt 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67206 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCACTCTCTAGACTTCTCCATCACGATGT 67147

Qy   1261 tacagccgaagctccgtcaagggtcctgtctcttcacctaccctgtatgctctac   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67146 TACAGCCAGAGCTCCGTGAGGGTCTGTCTTGTCTTCACACTTACCCTGTATGCTCTAC 67087

Qy   1321 acctgagctcactgcaactctgcctcccaggttcaagcaattctcctgtctctcagctc 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67086 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCCCTGTCTCAGCCTCC 67027

Qy   1381 cgggtagctgggactacagggcgcacggcctaattttgtattgttagtagagatggg 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67026 CGGGTAGCTGGGACTACAGGCGCACGGCCACCACGGCTAATTTTGTATTGTTAGTAGAGATGGG 66967

Qy   1441 gtttcaccatattagcccctggtcctgaactcctcagtgatctcacccaccctc    1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66966 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 66907

Qy   1501 agcccctaaagtgctgggattacaggcatgagtcacgcgcccggccaaggtcagtgt 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66906 AGCCTCCCAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGTCAGTGT 66847

Qy   1561 ttaataaaataacttgaatggttactacaacaaaagtcgtga                 1620
          |||||||||||||||||||||||||||||||||||||||||||
Db  66846 TTAATAAGGAATAACTTGAATGGTTTACTAAACACAGGCAGAAACAGAGAAAGTCTGTGA 66787

Qy   1621 taagttcagggatttctttgggaatgggggatggtgtcaatggcagctccaggac    1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66786 TAAGTTCAGGGGATTCTTGGGGATGGGGGATGGTGTGCCATGAGCTGCCTGCTGCCTAGTCCCAGAC 66727

Qy   1681 cactggttcctccatcacaacttctcctccatccattttcaggctaagttaccatttatt 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66726 CACTCGGTCCTCAATCACTTTCCATCCTCACTCATTTCAGGCTAAGTTACCATTTATT 66667

Qy   1741 caccatgtgtttgttgggttaggaagatttgggttaggtatacaataactag   1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66666 CACCAATGCTTTTGTTGGGTAAGCCCTCCACATCGTTACTGAAAATAAAGAGTATACATAAAACTAG 66607


Qy   1801 ttccatttggggccatctgtgtgtctgtatagggaggggggcataccccagagactcct 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66606 TTCCATTTGGGGCCCATCGTGTGTGTCTGTATAGGGAGGAGGGGCATACCCCAGAGACTCCT 66547

Qy   1861 tgaagcccccggcagagggtttcctctccagcagcagggtcc                 1920
          |||||||||||||||||||||||||||||||||||||||||||
Db  66546 TGAAGCCCCGGCAGAGGGTTTCCTCTCCCAGCTGGGGGAGGCACCCGGGGTCC 66487

Qy   1921 tgggtgtcctgagcaacctgccagcccgtgccactgggtgttctttgttcatcctctagg 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66486 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGGTGTTGTTTTGTTTATCCTCTAGG 66427

Qy   1981 gacctgttgcttctattttctgtgttcattcatcaggacctgacaatt          2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66426 GACCTGTTGCTTCTATTTTCTCATTTCTGTGTTCATTCATCAGGCAACACTGTGTTATCCACTCTCTAGG 66367

Qy   2041 tattgagtacttatatcctgcagacaccagaccagacaaaagtgagcaagtcactgc 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66366 TATTGAGTACTTATATCCTGCAGACACCAGACCAGACAAAAGTGAGCAAGTCACTGC 66307

Qy   2101 cctaccttcgtggagtgagagaccagttccagacaccagacaggagaaaattaatagcca 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66306 CCTACCTTCGTGGAGTGAGAGACCAGTTTCATGGGAAGAAAATTAATACCA 66247

Qy   2161 gccaaacttaaaccccagtgctgaaagaaataaacacaacatctttgaaagaaatttgtcgc 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66246 GCCAACTTAAACCCCAGTGCTGAAAGAAATAAACACAACATCTTTGAAAGAAATTTGTCGC 66187

Qy   2221 agcatccttaacaacaggccaacacctcccagcccccctgcctccacatcgtccgcgagg 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66186 AGCATCCCTTAACAACAGGCCAACACCTCCCAGCCCCCTGCCTCCACATCGTCCGGGAGG 66127

Qy   2281 cccccaaagacccgagtcttccaagcctcatccagtcacacgacgctggcct      2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66126 CCCCCAAAGACCCGAGTCTTCCAAGCCTCCACGTCTTCCATCAGTCAGCTGGCCT 66067

Qy   2341 gcctcgcttccccgtgaatcgtcctgtgctcattgcatctgagctccaaggct     2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66066 GCCTCGGCTTCCCGTGAATCGTCCTGTGCTCATCGCATCTGAGCTCCAGGCT 66007

Qy   2401 ccagaaaaggaaatggaggaagaactagttctaaaccgaaacaagctgcggtgttc  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66006 CCAGAAAAGGAAATGGAGGAAGAACTAGTTCTAAACCGAGAATCTGGAAGCGGTGTTTC 65947

Qy   2461 ctcagagggaagtgggcctccacgtcccagaagaagttccatgaggctgaggcagggag 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65946 CTCAGAGGGAAGGGCCTCCACGTCCCAGAAGAAGTCCATGAGGCTGAGGCAGGGAG 65887

Qy   2521 tggggacgcggggctgagcgggtgctgaagggaaagcagggaagggcaagttc     2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65886 TGGGGACGCGGGGCTGAGCGGGTGAGCGGGAAAGGCAGGGAAAGGGCAAGTGAA 65827

Qy   2581 gctgaccagatgttcagtgtgggccttccacgtgttcctgtctgagc          2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65826 GCTGACCAGATGTTCAGTGTGTTCACGGGCCTGGGAGTTCTCCGTTGCCTGTGAGC 65767

Qy   2641 cttcttttatctttgcttggaagggaagttctatttcatgaagtgatgcagttc   2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65766 CTTTTTTATCTTTCTGCTTGGAGGTTAAATTTCATTGAAGTGAGGGATGCAGTTTC 65707

Qy   2701 ataaagtcagctgttaaaaatttccaggttggttgtggttgggtcatttctttat 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65706 ATAAAGTCAGCTGTTAAAAATTCCAGGGTTTCCTTCACGGAGGCCTTTAT 65647

Qy   2761 ttaatgggaatatagaagcctcaatcattccatccgttaactctagcgaggaatggac 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65646 TTAATGGGAATATAGGAAGCTCAATCATTCCTAGCGTAACTCTAGGGTGTTTTCACGGAGGAATTGGAC 65587

Qy   2821 tggagtctttctttcatgtctttgggcaactactcagacccctggttgacttggctta 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65586 TGGAGTCTTTTCTTTCATGTCTTTGGGCAACTACTCAGACCCCTGGTGGACTTGCTTA 65527

Qy   2881 tgcaagacggtccgaaacctggaatcaggagagactcggtttcttctggtctgccatt 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  65526 TGCAAGACGGTCCGAAACCTGGAATCAGGAGAGACTCGGTTTCTTCTGGTCTGCCATT ...
```

```
Qy    5100  ccaaacagagacttctggaaggttattttctaagaaatcttgctgggcaaggcaacc   5159
            |||||||||| ||||||||||||||||| |||||||||||||||||| |||||||| ||
Db   63309  CCAAACAGACTTCTGGAAGGTTATTTTTCTAAGAAATCTTGCTGGCAAGGCAACCC    63250

Qy    5160  ccctgtgcacagcccaccaccagcctcacgtggccacctcgtcttccccccatgaaggct  5219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63249  CCCTGTGCACAGCCCACCACCAGCCTCACGTGGCCACCTCGTCTTCCCCCCATGAAGGCT  63190

Qy    5220  ggctaccccagtatatataaaacctctctcgggccagtgagccagccaaggccacccat   5279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63189  GGCTACCCCAGTATATATAAAACCTCTCTCGGGCCATGAGCCAGCCAAGGCCACCCAT    63130

Qy    5280  ccaggccaccctcagcgacagcgagagcgtttcaagagcctcaggctctgaatg       5339
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63129  CCAGGCACCCTTCAGCACCAGCAGCGAGAGCGTTTCAGAGAGAAGCCTCTGCAATG     63070

Qy    5340  aggttcttctgtgtcacgttcgtgctgcagcctttgggctttgggctggcctgctg      5399
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63069  AGGTTCTTCTGTGTCACGTTCGTGCTGCACCTTTGGGCTTTGGGCTGGCCTGCTG      63010

Qy    5400  ctttctggcctggcctgtgtgggcctgggcgccgggacagctcaggaaggccaat      5459
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63009  CTTTCTGGCCTGGCCTGTGTGGGCGGCGCCCAGGACAGCTCAGGAAGGCCAAT       62950

Qy    5460  gaccaggtggccgatgcccagtacccttcagtgtgtggccagtcccaatgaatccagctgc 5519
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62949  GACCAGAGTGGCCGATGCCCAGTATACCTTCAGTGTGTGGCCAGTCCCAATGAATCCAGCTGC 62890

Qy    5520  ccagagcagagccagcccatgtcatgtcatccatacattacagcagcagcagcaccca    5579
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62889  CCAGGACAGACCAGCCCAGTGTCAGTCATCAGCATCATTACAGCAGCAGCAGCACCAA    62830

Qy    5580  cgcttagacctggaggccacacaaagctcagtcagctcccctcacca               5639
            ||||||||||||||||||||||||||||||||||||||||||||||
Db   62829  CGCTTAGACCTGGAGGCCACCAAAGCTCAGTCCCTCTGGGAGAGCCTCCTCACCAA      62770

Qy    5640  ttgacctttgaccaggcctgccaggccccaggggcctgcagaggggactg           5699
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62769  TTGACCTTGGACCAGGCTGCCAGGCCCCAGGAGGGGCTGCAGAGGGGACTG         62710

Qy    5700  ggcaccctgaggcgggagagcgggaaccaagctggaaaaccaaaccagagagt         5759
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62709  GGCACCCTGAGGCGGGGGGACCCGGGACCAGCCTGCAAAACCAAACCAGAGACTGCC   62650

Qy    5760  tacaggcaaacctcctccgagacaaagtcaagtcctgggagaggaagcagctaaggcaa    5819
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62649  TACAGCAACCTCCTCCGAGACAAAGTCAAGTCTTCTGGGGAGGAAGCAGACTAAGGCA    62590

Qy    5820  gaaatgagaatctggccaggccaggcttggaaagcagcaggtagcaaggctgaga        5879
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62589  GAAAATGAGAAATCTGGCCAGGAGGTCCAGGAAAGCACAGAGGTTGGAGACTGCC       62530

Qy    5880  agggcccagtgttccccagagcccgagacacactcctgctgtgtgccccaggcgctccagagaa 5939
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62529  AGGGGCCAGTGTCCCCGGACACACTCCTCGGGCTGTGTGCCACCAGGGTTCCAGAA         62470

Qy    5940  ggtaagaatgcagagtggggggactctgagttcagcaggtgatatggctctgtagttgaccct 5999
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62469  GGTAAGAATCGAGAGTGGGGGGACTCTGAGTTCAGCAGGTGATATGGCTCTGTAGTTGACCT  62410

Qy    6000  gctacaggcggcctccaggcctc----cctgccctttcctcctagagagactgcacagctagcac 6055
            ||||||||||||||||||       ||||||||||||||||||||||||||||||||||
Db   62409  GCTACAGGCGGCCTCCAGGCCTCCTTTCTCTCCTAGAGACTGCACAGCTAGCAC          62350

Qy    6056  aagacagatgaattaaggaaagcaca-cgatcacctcaagtattactagtaattagct   6114
            ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db   62349  AAGACAGATGAATTAAGGAAAGCACACGATCACCTTCAGTATATTACTAGTAATTTAGCT   62290

Qy    6115  cctgagagcttcattagattaagtggttcagagttcttgtgccctccaatgtcag       6169
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62289  CCTGAGAGCTTCATTTAGATTAAGTGGTTCAGAGTTCTTGTGTGCCCTCCATGTCAG      62235
```

RESULT 2
AC024490

LOCUS   AC024490   170425 bp   DNA   HTG   26-MAY-2000
DEFINITION Homo sapiens chromosome 1 clone RP11-138F3 map 1, WORKING DRAFT
            SEQUENCE, 28 unordered pieces.
ACCESSION   AC024490
VERSION   AC024490.3 GI:8076950
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 170425)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE   Homo sapiens chromosome 1, clone RP11-138F3
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 170425)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M.,
            Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Illev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J.C., Landers,T., Largocque,K., Lehoczky,J., Levine,R.,
            Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
            McEwan,P., McKurk,A., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M.,
            Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
            Riley,R., Rogov,P., Roy,A., Santos,R., Schauer,S.,
            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
            Travers,M., Triglilo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
            Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
            Zody,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (28-FEB-2000) Whitehead Institute/ MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT   On May 25, 2000 this sequence version replaced gi:7249345.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------------- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            -------------------- Project Information
            Center project name: L7153
            Center clone name: 138_F_3
            -------------------- Summary Statistics
            Sequencing vector: M13; M7815; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.960731
            Consensus quality: 151483 bases at least Q40
            Consensus quality: 160439 bases at least Q30
            Consensus quality: 164708 bases at least Q20
            Insert size: 167000; agarose-fp
            Insert size: 167725; sum-of-contigs
            Quality coverage: 4.1 in Q20 bases; agarose-fp
            Quality coverage: 4.1 in Q20 bases; sum-of-contigs
            ----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 28 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will

* be preserved.
* 1 1300: contig of 1300 bp in length
* 1301 1400: gap of 100 bp
* 1401 2412: contig of 1012 bp in length
* 2413 2512: gap of 100 bp
* 2513 4147: contig of 1635 bp in length
* 4148 4247: gap of 100 bp
* 4248 5455: contig of 1208 bp in length
* 5456 5555: gap of 100 bp
* 5556 6997: contig of 1442 bp in length
* 6998 7097: gap of 100 bp
* 7098 8534: contig of 1437 bp in length
* 8535 8634: gap of 100 bp
* 8635 10164: contig of 1530 bp in length
* 10165 10264: gap of 100 bp
* 10265 10487: contig of 223 bp in length
* 10488 10587: gap of 100 bp
* 10588 12420: contig of 1833 bp in length
* 12421 12520: gap of 100 bp
* 12521 14843: contig of 2323 bp in length
* 14844 14943: gap of 100 bp
* 14944 17265: contig of 2322 bp in length
* 17266 17365: gap of 100 bp
* 17366 20071: contig of 2706 bp in length
* 20072 20171: gap of 100 bp
* 20172 23531: contig of 3360 bp in length
* 23532 23631: gap of 100 bp
* 23632 26137: contig of 2506 bp in length
* 26138 26237: gap of 100 bp
* 26238 29858: contig of 3621 bp in length
* 29859 29958: gap of 100 bp
* 29959 36225: contig of 6267 bp in length
* 36226 36325: gap of 100 bp
* 36326 44015: contig of 7690 bp in length
* 44016 44115: gap of 100 bp
* 44116 49493: contig of 5378 bp in length
* 49494 49593: gap of 100 bp
* 49594 56796: contig of 7203 bp in length
* 56797 56896: gap of 100 bp
* 56897 62860: contig of 564 bp in length
* 62861 62960: gap of 100 bp
* 62961 72552: contig of 9592 bp in length
* 72553 72652: gap of 100 bp
* 72653 83310: contig of 10658 bp in length
* 83311 83410: gap of 100 bp
* 83411 92992: contig of 9582 bp in length
* 92993 93092: gap of 100 bp
* 93093 103886: contig of 10794 bp in length
* 103887 103986: gap of 100 bp
* 103987 119418: contig of 15432 bp in length
* 119419 119518: gap of 100 bp
* 119519 136695: contig of 17177 bp in length
* 136696 136795: gap of 100 bp
* 136796 153977: contig of 17182 bp in length
* 153978 154077: gap of 100 bp
* 154078 170425: contig of 16348 bp in length.

FEATURES   Location/Qualifiers
source   1..170425
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /chromosome="1"
   /map="1"
misc_feature   /clone="RP11-138F3"
   /clone_lib="RPCI-11 Human Male BAC"
   1..1300
misc_feature   /note="assembly_fragment"
   1401..2412
misc_feature   /note="assembly_fragment"
   2513..4147
misc_feature   /note="assembly_fragment"
   4248..5455
misc_feature   /note="assembly_fragment"
   5556..6997

misc_feature   /note="assembly_fragment"
   7098..8534
misc_feature   /note="assembly_fragment"
   8635..10164
misc_feature   /note="assembly_fragment"
   10265..10487
   /note="assembly_fragment
   clone_end:SP6
   vector_side:right"
misc_feature   10588..12420
   /note="assembly_fragment"
misc_feature   12521..14843
   /note="assembly_fragment"
misc_feature   14944..17265
   /note="assembly_fragment"
misc_feature   17366..20071
   /note="assembly_fragment"
misc_feature   20172..23531
   /note="assembly_fragment"
misc_feature   23632..26137
   /note="assembly_fragment
   clone_end:T7
   vector_side:left"
misc_feature   26238..29858
   /note="assembly_fragment"
misc_feature   29959..36225
   /note="assembly_fragment"
misc_feature   36326..44015
   /note="assembly_fragment"
misc_feature   44116..49493
   /note="assembly_fragment"
misc_feature   49594..56796
   /note="assembly_fragment"
misc_feature   56897..62860
   /note="assembly_fragment"
misc_feature   62961..72552
   /note="assembly_fragment"
misc_feature   72653..83310
   /note="assembly_fragment"
misc_feature   83411..92992
   /note="assembly_fragment"
misc_feature   93093..103886
   /note="assembly_fragment"
misc_feature   103987..119418
   /note="assembly_fragment"
misc_feature   119519..136695
   /note="assembly_fragment"
misc_feature   136796..153977
   /note="assembly_fragment"
misc_feature   154078..170425
   /note="assembly_fragment"

BASE COUNT   48243 a   34101 c   34753 g   50621 t   2707 others
ORIGIN

Query Match   98.1%;   Score 6054.4;   DB 77;   Length 170425;
Best Local Similarity   99.6%;
Matches 6155;   Conservative   0;   Mismatches   11;   Indels   14;   Gaps   8;

```
Qy      1 atctttggttcagttta--cctcagggcgctattatgaaatgaaatgagaataaccaatgtgaa      58
          ||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db  63685 ATCTTTCGTTCAGTTTATCCTACAGGGCGCTATTATGAAATGAGAATAACCAATGTGAA       63744

Qy     59 agtcccataaactgttatagcctccatcg-gatgtatgtcttggcagg--atgataaag          115
          |||||||||||||||||||||||||||||| ||||||||||||||||||  |||||
Db  63745 AGTCCTATATACTGTATAGCCTCCATTCGTGAPGTATGTCTTTGGCAGGTATGTATAAAG    63804

Qy    116 aatcaggaagaaggagtatccacgttagccaagtgtccaggctgtgtcctgtcctcattt         175
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  63805 AATCAGGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGTCCTCTTATTT    63864

Qy    176 agtgacagaatgttgctcctgacagaggagctattcttcagggaaacatcaacatccaatatggt     235
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  63865 AGTGACAGATGTTGCTCTGACAAGAAGCTATTCTTCAGGAAACATCACATATGGT 63924
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    236 aaatccatcaaacaggagctaaggaaatgggacacttgcccaaggaaaat 295
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  63925 AAATCCATCAAACAGGAGCTAAGGAANTGGGACACTTGCCCAAGGAAAAAT 63984
Qy    296 gccaggagagcaaatatgatgaaaaatat.aattttcccttgttttaattcagaaa 355
Db  63985 GCCAGGAGAGCAAATAATGATGAAAAATAAACTTTCCCTTGTTTTAATTTCAGAAA 64044
Qy    356 aaatgatgaaggaccaaaatcaatgaatctcagaaagaaaagtgtttccaa 415
Db  64045 AAATGATGAAGGACCAAAATCAATGAATCTCAGAAAGAAAAGTGTTTCCAA 64104
Qy    416 attggtaattaagtatttgttcctttgggaggaaaagccatgtgactgagcttga 475
Db  64105 ATTGGTAATTAAGTATTTGTTCCTTTGGGAGGAAAAGCCATGTGACTGAGCTTGA 64164
Qy    476 gggaaaacgtcaaagtcaagctctgatcatgatcgatggatg 535
Db  64165 GGGAAAACGTCAAAGTCAAGCTCTGATCATGATCGATGGATG 64224
Qy    536 cagatggcatcactctgggaggaggcaagttcaggaagtcatgttagcaaagga 595
Db  64225 CAGATGGCATCACTCTGGGAGGAGGCAAGTTCAGGAAGTCATGTTAGCAAAGGA 64284
Qy    596 ataacagcaaatcaaaattccgaaatcgaggaggaaaatgtgggactgggaggaa 655
Db  64285 ATAACAGCAAATCAAAATTCCCGAAATCGAGGAGGAAAATGTGGGACTGGGAGGAA 64344
Qy    656 ataacagtgattaggcagttgaccatgttcgacaacactggggacttcc 715
Db  64345 ATAACAGTGATTAGGCAGTTGACCATGTTCGACAACACTGGGGACTTCC 64404
Qy    716 caaaaaattgactgggctaagcctggactttcaagggaaatataaaactgacgacaaa 775
Db  64405 CAAAAAATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATAAAACTGACGACAAA 64464
Qy    776 caaagagacatggttaaaggcaaccaccagagacaacattgtagctagggatg 835
Db  64465 CAAAAGACATGGTTAAAGGCAACCACCAGAGACAACATTGTGACCTGAAAGCAGCACTGCCCCT 64524
Qy    836 cagcaagggaccctgagcgcattttgccttaggaaggccagtttcttttcagaa 895
Db  64525 CAGCAAGGGACCCTGAGCGCATTTTGCCTTTAGGAAGGCCAGTTTCTTTTCAGAA 64584
Qy    896 aactctgaaaagatcagaaatctttaaccattttaagtatataaacaaatatgccatgcata 955
Db  64585 AACTCTGAAAAGATCATGAAATTTTAACCATTTTAAGTATAAAACAAATATGGCATGCATA 64644
Qy    956 atcagtttagacctgggtccccaatttttataagg tcaaggcatacaagtaacgtgtccca 1015
Db  64645 ATCAGTTTAGACTGGGTCCCCAATTTATAAGGTCAGGCATACAAGGATAAACGTGTCCCA 64704
Qy   1016 gctccggataggttcagaaatcattgagaaatcaactttttataaacttttcagaa 1075
Db  64705 GCTCCGGATAGGTTCAGAAATCATTAGAAATCACTGTCCCATCTAACTTTTCAGAA 64764
Qy   1076 tgatctgtctcacacacagccaggccgat gtgtctgactacaacactgtcacaacc 1135
Db  64765 TGATCTGTCATAGCCCTCACACAGGCCCGATGTGTCTGACTACAACACCATCACAA 64824
Qy   1136 cccaagtgcctcaacaccattgttaacgtgtctactcagaggtccaatgcacc 1195
Db  64825 CCCAAGTGCCTCAACCATTGTTAACGTGTCTACTCAGAGGTCCATCCAC 64884
Qy   1196 tcccctgtgcacagcctcccggctccacaagagagtctcccacactcagacttctgcatcac 1255
Db  64885 TCCCCTGTGCACAGCCATCCCGGCTCCACAAGAAGTCTCCCATCACTCAGACTTCTGCATCAC 64944
Qy   1256 gatgttacagccagagagctcctgtgagggtgagggtctgtgtcttacacctacctgtatgc 1315
Db  64945 GATGTTACAGCCAGAACCTCCTGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGC 65004
```

```
Qy   1316 tctacacctgagctcactcgcaacctctgcctcccagggttcaagcaaatctcctgcctcag 1375
Db  65005 TCTACACCTGAGCTCACTCGCAACCTCTGCCTCCCAGGTTCAAGCAAATTCTCCTGCCTCAG 65064
Qy   1376 cctccccgctagctgggactacaggcgcacgccggctaattttttgtatttttagtagag 1435
Db  65065 CCTCCCCGCTAGCTGGGACTACAGGCGCACGCCGGCTAATTTTTTGTATTTTTAGTAGAG 65124
Qy   1436 atggggtttcaccatattagccccggtctggtctcgaactcctgacctcaggtgatccacc 1495
Db  65125 ATGGGGTTTCACCATATTAGCCCGGTCTGGTCTCGAACTCCTGACCTCAGGTGATCCACC 65184
Qy   1496 acctcagcctcccaaagtgctggggattacaggcgtgagccacc 1555
Db  65185 ACCTCAGCCTCCCAAAGTGCTGGGGATTACAGGCGTGAGCCACC 65244
Qy   1556 agtgttaatggaataacctgaatggtttactaaaccaacaggaaacagaaaagc 1615
Db  65245 AGTGTTAATTAAGGAATAACTTGAATGGTTTACTAAACCAACAGGAAACAGAAAAGC 65304
Qy   1616 tgtgataatttcaggggaattcttgggatggggttcccatgtcctgacctctggctctcc 1675
Db  65305 TGTGATAATTTCAGGGAATTCTTGGGATGGGGTTCCCATGTCCTGAACCTCTGGCTCTCC 65364
Qy   1676 cagaccactggtcctccatcacttcttcccatccatccttccaggctaagttaccatt 1735
Db  65365 CAGACCACTGGTCCTCCATCAACTCTTCTCCCATCCATCCTTCCAGGCTAAGTTACCATT 65424
Qy   1736 ttattccacatgctctttgtgttagcctccacatcgttactgaataagagtatacatac 1795
Db  65425 TTATTCCACATGCTTTTTGTGGTAGCCTCCACATCGTTACTGAATAAGAGTATACATAA 65484
Qy   1796 actagttccattcattgggggccatctgctcagtctgcctgccaacctgccaactgtcc 1855
Db  65485 ACTAGTTCCATTTGGGGGCCATCTGCTCAGTTCTGCCACCTGGTCCCCAGTACCCCAGAGA 65544
Qy   1856 ctcttgaagtcccgcccgagaggtttctctccagccaagaagacacccgg 1915
Db  65545 CTCCTTGAAGGCAGCACCCGGTTTCTCTCCAGCTGGGGACCCTGCAAGGACGACCCGG 65604
Qy   1916 ggtcctgggtgttctggaggtgcacagttctcctggaggagtgtgttttctatcactct 1975
Db  65605 GGTCCTGGGTGTTCTGGAGGTGCACAGTTCTCCTGGAGGAGTGTGTTTTGTTTATCACTCT 65664
Qy   1976 ctaggggacctgtgctctcctattctgtgtgttcctatcgtttcttgtgtatgggaaatg 2035
Db  65665 CTAGGGGACCTGTTGCTTTCCTATTTCTGTGTGTTCCTATCGTTTCTTGTGTATGGGAAATG 65724
Qy   2036 caattctatttgatggactcattatctctgagccaagagacacaaagcaaggcagtc 2095
Db  65725 CAATTTATTTGAGTACTTATATATCTCCAGACAGACAAAATGGGTGAGCAAAGCAGTC 65784
Qy   2096 actgaccctacctcgtggaggtgacagttctctgggacagtcgcagagaaaaattaat 2155
Db  65785 ACTGACCCTACCTTCGTGGAGGTGACAGTTCTCAGTGACAAGTTCTGCAGAGAAAATTAAT 65844
Qy   2156 agccagccaaactaaaaacccagtgctgagaagaaataaaacacacttgaggaaattg 2215
Db  65845 AGCCAGCCAAACTTAAAAACCCAGTGGCTGAGAAGAAATAAAACCACATTGGAGGAAATTG 65904
Qy   2216 tgcgcagcaatccttaacaaagccaacctccttcccaagtcctcagcagtc 2275
Db  65905 TGCCGCAGCATCCCTTAACAAAGGCCACCCTCTTCCCAAGTCCTCAGCGCTGAGCT 65964
Qy   2276 ggaggccccaagccgagtcttccaagctcctccccagcccctgctgctgccactcagtgtcc 2335
Db  65965 GGAGGCCCCAAGCCCGAGTCTTTACAAGGCTCCTCCATCAGCTGCAGAGCCAGCT 66024
Qy   2336 ggccctgctcctgggctcggagactcctttgggctcc 2395
Db  66025 GGCCTGCTCCTGGAATCGTCCTTGGCTCC 66084
```

Qy   2396 aggcttccagaaagggaaatggaacggaggggggggacagt 2455
           ||||
Db   66085 AGGCTCCAGAAACGAAAATGAGGAGGGGAAACTAGTCTACGGAGAATCTGGAGGGGACAGT 66144

Qy   2456 gtttccctccagaggggaaagggggcctccacgtccaggagagaggaggaggggactgca 2515
           |||
Db   66145 GTTTCCTTCAGAGGGAAAGGGCCTCCACGTCCAGGAGGAATTCCAGGAGGGGGGACTGCA 66204

Qy   2516 ggggagtggggaggctgaacgcggggtgctcaagagcaaggcaagcaaggggggcaagt 2575
           |||
Db   66205 GGGGAGTGGGGGACCCTGGGGCTGAACGGGTGCTGAAAGGCCAGGAGGTGAAAAGGGCAAGG 66264

Qy   2576 gtttcataaagtcagctcgttaaaaattccaggtgttttccctgcttcctg 2635
           |||||
Db   66265 GTTTCATAAAGTCAGCTCTTAAAATTCCAGGTGTCATGGGTTCTTCCTG 66324

Qy   2636 tgagcctttatctttctctgcttgggagagagaagtctgggagtttcatgaagatgca 2695
           |||
Db   66325 TGAGCCTTTTATCTTTTATCTTTCTGCTTGGAGGAAAAGTCTGGGAGTTTCATGAAGGGATGCA 66384

Qy   2696 gtttcataaagtcaggtgttgtcatgggttgttttcctcacgaagggc 2755
           |||
Db   66385 AAGGTAAAGCCAAAACAGATTCAAAATTCCAGGTGTGCATGGGTTTCAGGAAGGCC 66444

Qy   2756 tttattttaatgggaatataggaggaagcgagctcattttcctctaggtccgttaattcacggagaa 2815
           |||
Db   66445 TTTATTTTAATGGGAATATAGGGAGTTCAGTTTGGTTGCGTTGCTTCG 66504

Qy   2816 gtggactgagtctttttttttttcatgtctctatttcatgggatgca 2875
           |||
Db   66505 GTGACTGGAGTCTTTTTATCTTTCTGCTTGGAGGAAGAGTCTATTTCATGAGGGGATGCA 66564

Qy   2876 gcttatgcaggtcggaaaacctttggaaatcaggagctggggtttttttctttgctcctg 2935
           |||
Db   66565 CTGCTATAAAGACCCTGCCAGCTCGTGTTCCTGTGGTTTTTCTTTTTCTGGTTCTG 66624

Qy   2936 ccaattggttggtgtgtgggcaagtgggcaagtctctctccttcccttgcccatagtctct 2995
           |||
Db   66625 CCAATTGTTGGGCTGTGCCAAGGTGTCTCTCCTTCCCTTGCCCATAGTCTTCT 66684

Qy   2996 ctgctatataagacccttgcaagtctctcgtctcttgaacattccactgg 3055
           ||||
Db   66685 CTGCTATAAAGACCCTGCCAGCTCTGGTCTCGGTGTTCCCTGGTGGACTTG 66744

Qy   3056 agggggatgttcagagggaaagggaaggcagctgagcagctgagcca 3115
           |||
Db   66745 AGGGGGATGTTCAGAGGGAAGGGGAAGGCAGGTTTTGGGGGGGAGGGTG 66804

Qy   3116 gagggggacagagaagctgggtgctccatcagtgatcaactca 3175
           |||
Db   66805 GAGGGGGACAGGAGGGCAGGAAGCTGGGTGCTCCATCAGTGATCACGGTCA 66864

Qy   3176 gactccaggaaccgagagcccaacagtgctcaatgaaccccaacagccaccacatt 3235
           |||
Db   66865 GACTCCAGGACCGAGAGCACAATGCTCAGGAAAGCTCAATGAACCCAACAGCCCACATT 66924

Qy   3236 ttcctttccctaaggcatggtcaataccaaacaatgcagagactaa 3295
           |||
Db   66925 TTCCTTCCCTAAGGCATGGTCAATAACCAAAAAGAAGAAATGCAGAGACTAA 66984

Qy   3296 ctggtgtgtagctcttgctgctggccaagtcaaagatgccaga 3355
           |||
Db   66985 CTGGTGGTAGCTTTTTGCCTGGCCATTCAAAAACTGGCCAGAGAAATGCCAGA 67044

Qy   3356 gattgttaaacttttcacccctgaccacgcccgcagctcagcacgcccaga 3415
           |||
Db   67045 GATTGTTAAACTTTTCACCCTGACCGTGGGAAGCTGGGTGCTCCATCAGTGATCACGTCAG 67104

Qy   3416 cacggagtgactcagcaggggagagagagtagtgtatgagcaa 3475
           ||||
Db   67105 CACGGAGTGACCTGCACCGCCCAGCGCCCAGGGGAGAGAGAAGAGAGGGATACTGTATGAGCAA 67164

Qy   3476 gaaagacagattcattcaaggcagtgggaattgaccacccaggagttatagtccacgtgat 3535
           |||
Db   67165 GAAAGACAGATTCATTCAAGGGCAGTGGGGAATTGACCACCAGGGATTATAGTCCACGTGAT 67224

Qy   3536 cctgggttctagggagaggcaggggctatatgtgtgggggggaaaatcagtgaaagtcg 3595
           |||
Db   67225 CCTGGGTTCTAGGGAGAGGCAGGGGCTATATTGTGGGGGGGAAAATCAGTGAAAGTCG 67284

Qy   3596 ggagacctgacttctctaatacttactatattttcccttacaagctgagtaactcctgagcaagtc 3655
           |||
Db   67285 GGAGACCTGACTTCTCTAAATACTACTATATTTTCCCTTACAAGCTGAGTAGTTCCTGAGCAAGTC 67344

Qy   3656 acaaggtagtaactgaggcgtagaattacttactgttctcctttc 3715
           |||
Db   67345 ACAAGGTAGTAACTGAGGCGTAGAATTACTTACTGTTTTTC 67404

Qy   3716 tctgtgggttagcagcaagggcaaagggctctttcttctccttacaggatcct 3775
           |||
Db   67405 TCTGTGGGTTAGCAGCAAGGGCACAAGGGGCAATCCCGTTTCTTTTTAACAGGGAAAGACAATTCCT 67464

Qy   3776 aagagtaaagccaaacagattccaagcctaggctctagtagtctct 3835
           |||
Db   67465 AAGAGTAAAGCCAAAACAGATTCCAAGCCTAGGCTCTAGTAGTCTCT 67524

Qy   3836 aaaatcattcagcgatgttttactcttcacagggtc 3895
           |||
Db   67525 AAAATCATTCAGCGATGTTTTACTTTCACAAAAATGAGACCCTTGGGTC 67584

Qy   3896 agctgtaacacaaacaccagttggaaaatattacttcacaagtctaactaacaat 3955
           |||
Db   67585 AGCTGTAACACAAACCCCAGTTGGAAAAATATTACTTCACAAGTTTAACTAACAAT 67644

Qy   3956 caaa-aagaatagaatctttagagcaaactgttgttctcccacactctgggagtgagtctgc 4014
           ||||
Db   67645 CAAATAAGAATAGAATCTTTAGAGCAAACTGTTGTTTCTCCAC-TCTGGAGGTGAGTCTGC 67703

Qy   4015 cagggcagttgggaaatattttcacccaagttttgtctgtaggtattaacacca 4074
           |||
Db   67705 CAGGGCAGTTGGAAATATTTCACCCAAGTGTTTACTCTGTAGTATTAACACA 67763

Qy   4075 taaagttgtcaaagcaatcattaattatcacaagtctaactaacaat 4134
           |||
Db   67765 TAAAGTTGCTCAAAGCAATCATTAATTATTCAAGTTAACTAGTAACCAAT 67823

Qy   4135 gtatatttattggctcattgcattttgctttttgttttttctctctgc 4194
           |||
Db   67824 GTATATTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTGGGTTTATTAATGTA 67883

Qy   4195 aagcaggggattatacccagtgaatttgaatgagggaaggaatta 4254
           |||
Db   67884 AAGCAGGGGATTATTAACCTAGGGTCCAGGAAAGCCTGGAATGGAGGAAAAAATTA 67943

Qy   4255 cattttgttctttaccccttctcaactaaattacaattttatcttgtatctta 4314
           |||
Db   67944 CATTTTGTTCTTTACCCTTCTCAACTAAAATTAATAATTTATTCTTGTATAGAGC 68003

Qy   4315 cataaaactcaaagtgtaataaccagtacccgtgattctgttaccaatcaca 4374
           |||
Db   68004 CATAAAACTCAAAGTGTAATAACCAGTACCCGTGATTCCATTGCCAATCACA 68063

Qy   4375 gacatttatactatattacacttgcagatagttgaagtacactca 4434
           |||
Db   68064 GACATTTTTATACTATATTTACAGTTGCAGATAGGTTGTTGAATTTATACTCA 68123

Qy   4435 aaaatactttgaaattggaaattagaactcccctgctgggatctcttggatcttgtcagaa 4494
           |||
Db   68124 AAACTACTTTGAATTTGAAATTAGAACCTCCCTGCTGGATCTCTTGTTTAACATATATAAAAACATG 68183

Qy   4495 tttaaaatcttgatattttgataatcatattcattgttctcctttgtatctta 4554
           |||
Db   68184 TTTAAAAATTTTGATATTTTGATAATCATATTCATTATATCATTTGTTGTAATCTA 68243

Qy   4555 tattttatatttcgaaaacaatctttctggagagaagttccaatgaggt 4614
           |||

```
Db  68244  TATTTATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCAGATTTCACCAATGAGGT       68303
Qy   4615  tcttggacatgcacacacagagtaagaactgatttagaggctaacattggttgc          4674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68304  TCTTGGCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGGTGC            68363
Qy   4675  ctgagaatgcaagactgaaatttgttcctcccaaagatacacagttgtttaaagcta       4734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68364  CTGAGAATGCAAGACTGAAATTTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTA   68423
Qy   4735  gggtgtgaggggggaaatctccgccttctatgagccctggttggggt                 4794
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  68424  GGGGTGTGAGGGGGGAAATCTCCGCCTTCTATGAGCCCTGGTTAGGGT                68483
Qy   4795  gctgcgttccttcgttctggctggctggctggcgcttcctctctctgctcctaaggac      4854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68484  GCTGCGTTCCTTCGTTCTGGCTGGCTGGCTCCCGCTTCCTCTCTCTGCTCCTAAGGAC      68543
Qy   4855  ttgtttgggatctcagggtttcatcatcctctacggctcttccaatgagtt             4914
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68544  TTGTTTGGGATCTCACAGTTTCATCATCCTCTACGGCTCTTCCAATGAGTTT            68603
Qy   4915  gcaagagtgaatggaaatataaactagaacactagacagcacacagtag               4974
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68604  GCAGAGTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAG    68663
Qy   4975  tcctggttgtgttgtacggctgtgtgtgtgtgtgtgaaaaccaggtg                 5034
           |||||||||||||||||||||||||||||||||||||||||||||||
Db  68664  TCCTGGTGTTAAGTGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGAAAACCAGGTG        68721
Qy   5035  gagataggagaactattatttggggatgatgtgttcttttttaaaaag                5094
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  68722  GAGATATAGGAGAACTATTATTTGGGGTATGGGTGGTGCATAAATGTGTTCTTTTTAAAAAG  68781
Qy   5095  aaactccaaacagacttctgggaaggttattttctgtggcagctgaagc               5154
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  68782  AAACTCCAAACAGACTTCCGGAAGGTTTATTTTCTAAGAAATCTTTGCTTGGCAGGC       68841
Qy   5155  aacccccctgtgcaacagcagcgcttcacagtcaacctcactctccccatgaa           5214
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68842  AACCCCCTGTGCACAGCCCACGTCCAGCCTCTGTCTTCCCCCCTCTGTAA              68901
Qy   5215  gggctggctccccagtatatataaaacctctcgggctcgggcatgagc                5274
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  68902  GGGCTGGCTCCCCAGTATATATAAAACCTCTCGGGCATGAGCCTCGGGGGCATGA         68961
Qy   5275  cccatccaggcacacctcagcacagcagcgcttcacagcctcacccagagcctcacctg     5334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68962  CCCATCCAGGCACACCTTCACCACACCAGCTTTCACGAGGAAGCCTCTCACCAAGCCTCTG   69021
Qy   5335  caatgagggtcttctgtcacgttgctcagcttggggctgagatgccagctgccagc        5394
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69022  CAATGACAGAGTGTCCGCAGTATACCTTCAGTGTGGCCACGTGTGTGGCCAAATGAATCCA   69081
Qy   5395  tgctgcttctggcctggtgttgggatgtgggggccaggaagg                      5454
           ||||||||||||||||||||||||||||||||||||||||||
Db  69082  TGCTGCTTCTGGCCTGGTGTTGGGATGTGGGGGCCAGGACAGCAGCTCAGGAAGG         69141
Qy   5455  ccaatgaccagagagtgccatggccatgtcccatgcca                          5514
           ||||||||||||||||||||||||||||||||||||||
Db  69142  CCAATGACCAGAGAGTGCCGATGCCAGTATACCTTCAGTGTGTGGCCAATGAATCCA       69201
Qy   5515  gctgcccagagagaggccaggccatgccatcagcagcagca                       5574
           |||||||||||||||||||||||||||||||||||||||||
Db  69202  GCTGCCCAGAGAGAGCGGCCAGGCCATGTCAGTCATCCATAACTTCAGAGACACAGCA      69261
Qy   5575  cccaacgcttagacctgggggcccacaaagctcgctcctc                        5634
           ||||||||||||||||||||||||||||||||||||||||
Db  69262  CCCAACGCTTAGACCTGGAGGCCCACCAAAGCTCACTCCTCC                      69321
Qy   5635  accaattgaccttgaccagggctgccagc                                   5694
           |||||||||||||||||||||||||||||
Db  69322  ACCAATTGACCTTGACCAGGCCTGCCAGGGG                                 69381
```

```
Qy   5695  agctgggcacctgagcgcgggacggaccagagctcggaaaccaaaaccacgagagtggaga  5754
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69382  AGCTGGGCCACCCTGAGGCGCGGAGCGGGGCCAAAAAACCCAGAGGTTGGAGA           69441
Qy   5755  ctgcctacagcaaccctcctccgagacaagtcagttctggaggaagaagcgactaa       5814
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69442  CTGCCTACAGCAACCTCCTCCGAGACAAGTCAGTTCTGGAGGAAGAAGCGACTAA         69501
Qy   5815  ggcaagaaaatgagaatctggccagaggaggttgagaaagcaggcagaggagtagaaaggc  5874
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69502  GGCAAGAAAATGAGAATCTGGCCAGAGGAGGTTGGGAAAGCAGGCAGAGGAGTAGAAAGGC   69561
Qy   5875  tgagaagggggccagtgtcccagagagacacgtctcggggctgtgccacaggggtcca     5934
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69562  TGAGAGAGGGGCCAGTGTCCCAGAGAGACACGTCTCGGGGCTGTGCCACCAGGGGTCCA     69621
Qy   5935  gagaggtaagagttcagaagacactggaaagcagagacactcttggaaagcagagtttt    5994
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69622  GAGAAGTAAGAATGCAGGAAGTTGGAAAGCAGAGACACTCTTGGAAAGCAGAGTTT        69681
Qy   5995  gacctgctaagggcgctccagggcccctttctctcagcctgagttcacgtgatatggctcttgt  6050
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69682  GACCTGCTACAGGGCGCTCCCGCCCTTTCTCCTAGAGACTGCGCACAGCT              69741
Qy   6051  agcacagacagagtgaattaaaggaaagcaca-cgatcaccctcaagtatatactagtaatt  6109
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  69742  AGCACAAGACAGATGAATTAAGGAAAAGCACACGATCACCTTCAAGTATTACTAGTAATT    69801
Qy   6110  tagctcctgagagcttcatttagattagttggttcaagagttcttgtgccccctccagtcag  6169
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  69802  TAGCTCCTGACAGCTTCATTTAGATTAGTGTTCAAGAGTTCTTGTGCCCCCATGTCAG      69861
```

BASE COUNT   1483 a   1152 c   1236 g   1429 t
ORIGIN

Query Match
Best Local Similarity 100.0%;   Score 5300;   DB 11;   Length 5300;
Matches 5300;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Pred. No. 0;

```
Qy      1 atctttgttcagtttacctcagggcgtattatgaaatgaaacaaatgtcgaaag    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCTTTGTTCAGTTTACCTCAGGGCGTATTATGAAATGAAACAAATGTCGAAAG    60

Qy     61 tcctataaactgtatagcctccatcctcgggtctgtatgtctttcgggcagagatgaatga   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCTATAAACTGTATAGCCTCCATCCTCGGGTCTGTATGTCTTTCGGGCAGAGATGAATGA   120

Qy    121 ggaagaaggagtatcccagttagccaagtgtccagggctgttgtctctcttattttagtga   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAGAAGGAGTATCCCAGTTAGCCAAGTGTCCAGGGCTGTTGTCTCTCTTATTTTAGTGA   180

Qy    181 cagatgttgtcctgacaagaagctattcttcaggagaaacacatcacatcacaatggtaaatc   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CAGATGTTGTCCTGACAAGAAGCTATTCTTCAGGAGAAACACATCACATCACAATGGTAAATC   240

Qy    241 catcaaacaggagagctaagaaacaggaatgggcacttgcccaaggaaggaaaatgccag   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CATCAAACAGGAGAGCTAAGAAACAGGAATGGGCACTTGCCCAAGGAAGGAAAATGCCAG   300

Qy    301 gagagcaaaataatgatgaaaaataaactttcccttttgtttttaattcaggaaaaaatg   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAAATAATGATGAAAAATAAACTTTCCCTTTTGTTTTTAATTCAGGAAAAAATG   360

Qy    361 atgaggaaccaaaatcaatgaataaggaaaaactctccacctgtgactccatgtgagctgac   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGAACCAAAATCAATGAATAAGGAAAAACTCTCCACCTGTGACTCCATGTGAGCTGAC   420

Qy    421 taattaagtatattgttctcctgggaagagagatctccaatgcttgatggtttccaaaatgg   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATATTGTTCTCCTGGGAAGAGAGATCTCCAATGCTTGATGGTTTCAAAATGG   480

Qy    481 aaacgtcaaaagcatgatctgatcagatcccaagtggaattcattattttaaaaaccagat   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGGAATTCATTATTTTAAAAACCAGAT   540

Qy    541 ggcatcactctgggagggcaagttcatgttagcacataacaataac   600
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGAGGGCAAGTTCATGTTAGCACATAACAATAAC   600

Qy    601 agcaaaatcaaaatcccgcaaaatgcagaggaaaaatgggactggaaagcttcataag   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAAATCAAAATCCCGCAAAATGCAGAGGAAAAATGGGACTGGAAAGCTTCATAAC   660

Qy    661 agtgattaggcagttgaccatgtttcgacaacacctcccgtctataccaggggaacacaaa   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGACCATGTTTCGACAACACCTCCCGTCTATACCAGGGGAACACAAA   720

Qy    721 attgactgggctaagcctccaagggaaatatggaagaacaacataac   780
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTCCAAGGGAAATATGAGAGCAAAACAAAA   780

Qy    781 gacatggttaaaaggcaaccacacaagttgtgaccctccaaacagaccagca   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGGTTAAAAGGCAAACCACACAAGTTGTGACCCTCCAAACAGACCACCA   840

Qy    841 gggaccctgaggccattgcccttaggaaggccagtttttcttaaggaataactc   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCCATTGCCCTTAGGAAGGCCAGTTTTTCTTAAGGAATCTTAAGGAAAGCTC   900

Qy    901 ttgaaagatcatgaatctttaaccatcttaagtataaacaaatatggatgataatcag   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAACAAATATGGGATGATAATCAG   960

Qy    961 tttagacatgggtcccaatttatataagtcaggcatacaaggaataacgtgtcccagctcc   1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAAGCTGTCCCAGCTCC   1020

Qy   1021 ggataggtcaggaaatcattaggaaatactgtgtcccatcctaacttctttcaggaatgatc   1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGATAGGTCAGGAAATCATTAGGAAATCACTGTGTCCCATCCTAACTTTTTCAGGAATGATC   1080

Qy   1081 tgtcatagcccctcaaccatcccgtctccaacaggcccgatgtgtctgacctacaaccaactctacaaaccaa   1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GTCCTCAAACCATTGTTAACGTCACACACAGCCCCGATGTGTCTGACCTACTTGCACTACAACTCTACAACCAA   1140

Qy   1141 gtggctcaaccattgttaacgtgtcatctcagtagggtccagttatcaacctgatagtcacgtgt   1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAAACCATTGTTAACGTGTCATCTCAGTAGGGTCCCACTTAGACTTCTGCATCTACAAAATGCCACTTCCC   1200

Qy   1201 tacagccagaagctccgtgagggttgagggtctgtgtcttacacccttactagctcttac   1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TACAGCCAGAAGCTCCGTGAGGGTTGAGGGTCTGTGTCTTACACCCTTACTAGCTCTTAC   1260

Qy   1261 acctgagctcactgcaactctgccctccaggtccaagcaattcctcctgtcctcagcctc   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ACCTGAGCTCACTGCAACTCTGCCCTCCAGGTCCAAGCAATTCCTCCTGTCCTCAGCCTC   1320

Qy   1321 cgcgtagctgggaactacaggcgcacgcccggtccggccggccggccaagggtcagtgt   1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG   1380

Qy   1381 ttaataggaaataacttgaaatctgaatggtttactaaaacaacagggagaaactcag   1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACCGCATGGGCCCAAGGGTCAGTGT   1440

Qy   1441 gttccacatcattagccccgcgtggggtcctggaacctgatcatccacccaactc   1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTAATAAGGAATAACTTGAAATGGTTTACTAAAACAACAGGGAGAAACTCTGA   1500

Qy   1501 agcctcctaaagtgctgggattacaggcgtgagccaccgcatgggccaaggggtcagtgt   1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACCGCATGGGCCAAGGGGTCAGTGT   1560

Qy   1561 ttaataaggaataacttgaaatggtttactaaaacaacagggagaaactctga   1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTAATAAGGAATAACTTGAAATGGTTTACTAAAACAACAGGGAGAAACTCTGA   1620

Qy   1621 taatttcaggggattcttgggatggggaatggtgccatgaagctgtcctagtcccagac   1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TAATTTCAGGGGATTCTTGGGATGGGGAATGGTGCCATGAAGCTGTCCTAGTCCCAGAC   1680

Qy   1681 cactggttcctcatcaacttcctccttccatcttcaggtcaagtttacacatttatt   1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTGGTTCCTCATCAACTTCCTCCTTCCATCTTCAGGTCAAGTTTACACATTTTATT   1740

Qy   1741 cacccatgctcttgtgtaagcctccaacatcgtcaacctacagttactgaaataacaactaaaatcg   1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CACCATGCTCTTTGTGGTAAGCCTGTTCATCACTTTCTCCCCATCTTCAGGGTTACTGAAATAGGTATACAAAACTAG   1800

Qy   1801 tcccatttgggggcaatctgctgtgtgtgtgtatagggactggggactct   1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTCCCATTTGGGGCCATCTGCTGTGTGTGTATAGGGAGGGGGTCC   1860

Qy   1861 tgaagcccccgagagtttcctctctccctgcaagcaccccggggtcc   1920
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGAAGCCCCCGAGAGTTTCCTCTCTCCCTGCAAGCACCCCAGAGCTCC   1920

Qy   1921 tgggtgtcctgagcaactgccactgttgttctatcactctagg   1980
          |||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGGTGTCCTGAGCAACCTGCCACCCGTGCCAATGGTGTTTATCACTCTCTAGG   1980

Qy   1981 ttgaaagaatcatgaattttaactatttctgtgactcgttcaatcaatcatgaacaatt   2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GACCTGTTGCTTCTTATTTCTGTATTTCATTCATTCAGGTCATTGACAAATT   2040

Qy   2041 tattgagtactattatccgcacagacacagagacaaaatgtcgagcaaagcagtcactgc   2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TATTGAGTACTATTATCCGCACAGACACAGAGACAAAATGTCGAGCAAAGCAGTCACTGC   2100
```

Db 2041 TATTGAGTACTTATATCTCCAGACCAGAGACAAAATGGTGAGCAAAGCTCACTGC 2100
Qy 2101 cctacccttcgtggaggtgacagtttcctccatggaagacgtgcagaagaaattaatagcca 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCACATGGAAGACGTGCAGAAGAAATTAATAGCCA 2160
Qy 2161 gccaacttaaacccagtgctgaagaagaaagaacccattctgaagagtat tgtgcgc 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAGAAGAAATAAACCATACTTGAGAGAATTGTGCGC 2220
Qy 2221 agcatccttaacaaggccacctcccctccctagcgccccatcgtgcccgaagg 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCCTAGCGCCCCATCGTGCCCGGAGG 2280
Qy 2281 ccccaagcccagtcttccaagcctcagctggcct 2340
Db 2281 CCCCAAGCCCGAGTCTTCCAAGCCTCAGCTGGCCT 2340
Qy 2341 gcctctgcgtcctcccgtgaatcgtggtgtctggctggctcctctctccatcagcgctcccaggct 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGTCGACTCGACTCCTGGCTCCAGGCT 2400
Qy 2401 ccagaaaggaaatgtgagaaggggaaactagtctaacggagagaggaaacagtgtttc 2460
Db 2401 CCAGAAAGAGGAAATGTGGAGAGGGGGAAACTAGTCTAACGGAGAGACAGTGTTTC 2460
Qy 2461 ctcaagaggaaaggggccccacccagtccaggaagaattccaggagggctgcaggag 2520
Db 2461 CTCAGAGGGGAAAGGGGCCCACGTCCAGGAAATTCCAGGAGGGCTGCAGGGAG 2520
Qy 2521 tggggaccgctgggggctggagcgggtgctgggaggagggcaggagggctgaa 2580
Db 2521 TGGGGACGGCTGGGGCTGAAAGGCAGGAGGGCAAGGCTGAA 2580
Qy 2581 gctgcccagtgttcagtgctgttgtctccgttcccggggctgggagttttccgtgtgctcctgtgagc 2640
Db 2581 GCTCCCCAGATGCTGGGGGTCCACGGGTGCTGAAAGGCAAGCTCAGGGAG 2640
Qy 2641 cttttatctttctctgctctggagagagaagtctatttctatggatgcaggttc 2700
Db 2641 CTTTTATCTTTCTCTGCTCTGGAGAGAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ataaagtcaagctgttaaaattcaggggtttgcatggtttttcttccagggtttcacatgg 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCAGGGGTGTGCATGGGTTTTCTTCCACGGGTTTCACATGG 2760
Qy 2761 ttaatgggaatataggagacgcagtcattctccggggccgttaattcacggaaggaagtgac 2820
Db 2761 TTAATGGGAATAATAGGAACGGAGCTCATTTCCTAGGCGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 tgggtctcttctcttcatgtctctgggccaactactcagccctgtggttggactgggctta 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCCAACTACTACACCCCTGTGGTGGACTTGGGCTTA 2880
Qy 2881 tgcaagaggctcgaaaaacctttgaatcagagactccggttttcttcttttcctgccatt 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAAATCAGGAGACTCGGTTTTCTTTCTTTTCCTGCCATT 2940
Qy 2941 ggttggctcgtgtgcgaccgtgggcaagtgtctctctcttcctgggccatagtagtctctctgct 3000
Db 2941 GGTTGGCTGTGTGCGACCGTGGGCAAGTGTCTCTCGTGACACTTCCTGTGTCTCTGTGAGGGG 3000
Qy 3001 ataaagaccttgcagctctcgttctgtgaccacttccctgttaattcctgacccttgggggg 3060
Db 3001 ATAAAGACCCTTGCAGTCTCGTGTCTTGTGACACTTCCTGTGATTCTGTGAGGGG 3060
Qy 3061 ggagtgttctgaagccgtcgaggagcacaaagctgggagagagagg 3120
Db 3061 GGATGTTGAGAGGGAAGGGGAAGGCAGAGGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 ggacaggagaaggcaggcgaaagctcgggtgtgctccatcagtcctcactgatcaacgtcagaactc 3180
Db 3121 GGACAGGAAGCAGGCAGGCGAAAGCTCGGGTGCTCCATCAGTCCTCACTGATCAACGTCAGAGACTC 3180

Qy 3181 caggaccgagagcacaatgctcaggggaaaagctcaatgaaccaacaagcaccacattttcct 3240
Db 3181 CAGGACCGAGAGCACAAATGCTTCAGGGAAAAGCTCAATGAACCCAACAGCACCACATTTTCCT 3240
Qy 3241 tccctaagcatagaacatggacatttgccaataacaaaagaatgcagaagactaactggt 3300
Db 3241 TCCCTAAGCATAGAGACATGGCATTTGCCAATAACAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 ggtagcttttgtcgggccattcaaaacaaaagctgggaatggaagctgggaaaattg 3360
Db 3301 GGTAGCTTTTGCCGGGCCATTCAAAAACTGGGAATGGAAGCTGGGAAAATTG 3360
Qy 3361 ttaaacttttcacccctgaccagcagcccacccccacgccagctcagcagctgacagccacgg 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCAGCCCACCCCCACGCCAGCTCAGCAGCTGACAGCCACGG 3420
Qy 3421 agtgacctgcagcgcaggggggaggagggagagagagtagtgtatggacaagaaag 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAGAGAGAGAGTAGTGTATGGACAAGAAAG 3480
Qy 3481 acaagattcattcaaggcacaggggaattgacccacagctgggagaattagctagcctggtgtcctgg 3540
Db 3481 ACAGATTCATTCAAGGCACAGGGGAATTGACACACAGCTGGGAGAATTATAGTCCACGTGATCCTGG 3540
Qy 3541 gttcctaggagggcaggggcctatcttgtgggggggaaaaatcagttcaagggaagttcgggaga 3600
Db 3541 GTTCCTAGGGAGGGCAGGGGCCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTGGGGGAGA 3600
Qy 3601 cctgattctaatacatactatttttccctttaagctgagtgaattctgacgaagtcacaag 3660
Db 3601 CCTGATTCTAATACATATATTTTTCCCTTTAAGCTGAGTGAATTCTGACGAAGTCACAAG 3660
Qy 3661 gtagtaactgagtgctgtaaggattacttacttagttctttctccctttaacagctgaag 3720
Db 3661 GTAGTAACTGAGTGCTGTAAGGATTACTTACTTAGTTCTTTCTCCCTTTATTAGGAAAGCTGAAG 3720
Qy 3721 ggagttagtagcacagagggccaatcccggttttctttctttaacaggaagaacagttttctctgt 3780
Db 3721 GGAGTTAGTAGCACAGAGGGCCAATCCCGGTTTTCTTTCTTTTTAAACAGGAAGAACATTCCTAAGAG 3780
Qy 3781 taaagccaaacagattcaagcctagttctgctgaactctatgattggtcttctgaaaat 3840
Db 3781 TAAAGCCAAACAGATTCAAACCCTAGCTCTTGCTGAACTCTATGATTGGTCTTTTGAAAAAT 3840
Qy 3841 cattccaggcgatgttctactatctcaatttctcagaaaatgagactagtaacccttggtcaggg 3900
Db 3841 CATTTCAGGCGATGTTTCTACTATCTCAATTTCAGAAAATGAGACTAGTAACCCTTGGTCAGGGCTG 3900
Qy 3901 taaacaacaccccagttgtaaatgttctcaagttcaagtggaccaatcaaaa 3960
Db 3901 TAAACAAAACACCCAGTTGTAAATGTTCTCAAGTTCAAGTTGGACCAATCAAAA 3960
Qy 3961 agaatagaatctttagagcaaaactgtgttcttctccacactctggagtgtctgccaggggc 4020
Db 3961 AGAATAGAATCTTTAGAGCAAAACTGTGTTTTTCTCCACATCTGGAGTGTCTGCCAGGGC 4020
Qy 4021 agttggaaatatatttacttcacacagtatgcagacaacacataaagt 4080
Db 4021 AGTTGGAAATATTTACTTCACACAGTATGCAGACAAACATAAAGT 4080
Qy 4081 tgctcaaggcaatcatttattgcttaagtgggttaaagttacttcgacagtttttatat 4140
Db 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCGACAGTTTTTGTATAT 4140
Qy 4141 ttattggctattgccattgctttgtcttttgttttacttattaatgtaaagcag 4200
Db 4141 TTATTGGCTATTGCCATTTGCTTTGTCTTTGGTTTATTAATGTAAAGCAG 4200
Qy 4201 ggattattaacctaccagtccagaagaagcctgtgaatttgaattgagaaaatttacattt 4260
Db 4201 GGATTATTAACCTACCAGTCCAGAAGAAGCCTGTGAATTTGAATTGAGGAAAATTACATTTT 4260

```
RESULT   4

HSMYOC1
LOCUS       HSMYOC1      2800 bp    DNA              PRI       21-APR-1998
DEFINITION  Homo sapiens myocilin (GLC1A) gene, promoter and exon 1.
ACCESSION   AF049791
VERSION     AF049791.1  GI:3065670
KEYWORDS    .
SEGMENT     1 of 3
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2800)
  AUTHORS   Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
            Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
  TITLE     Characterization and comparison of the human and mouse GLC1A
            glaucoma genes
  JOURNAL   Genome Res. (1998) In press
REFERENCE   2  (bases 1 to 2800)
  AUTHORS   Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
            Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-1998) Ophthalmology, University of Iowa, 200
            Hawkins Drive, Iowa City, IA 52242, USA
FEATURES             Location/Qualifiers
     source          1..2800
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q21-q31"
     promoter        1..1905
     exon            1906..2509
                     /gene="GLC1A"
                     /number=1
BASE COUNT      781 a    588 c    673 g    758 t
ORIGIN
```

```
Query Match             43.4%;  Score 2677.4;  DB 66;  Length 2800;
Best Local Similarity   99.7%;  Pred. No. 0;  Mismatches 1:  Indels 8:  Gaps 5:
Matches 2736;  Conservative 0;  Mismatches 1:  Indels 8:  Gaps 5:

Qy  3431 agcgcagggggaggagaagaaaaaagaggagaaagtagtgtatcgacaagaaagacagttcat 3490
         ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db     1 AGCGCAGGGGGAGGAGGAAG--AAAAAGAGGAGAAAGTAGTGTATCGACAAGAAAGACAGATTCAT 59

Qy  3491 tcaagggcagtggggaaattgaccacagcagggaatta...tagtccacgtgatcctggggttctaggag 3550
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    60 TCAAGGGCAGTGGGGAATTGACCACCAGCAGGGAATTATAGTCCACGTGATCCTGGGTTCAGGAG 119

Qy  3551 gcaggggctatattgttggggggaaaaacaagtcaacaaaggagaagtcggagacctgatttct 3610
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 GCAGGGCTATATTGTTGGGGGGAAAAATCAGTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy  3611 aatacatatattttccctttacaagctgagtaatctggagcaaggtcacacaaggtagtaactg 3670
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 AATACTATATTTTTCCCTTTACAAGCTGAGTAATCTCGAGCAAGGTCACAAGGTAGTAACTG 239

Qy  3671 aggctgtaaggattagtttctccctcctattaggaaactctttctctctgtggagttagca 3730
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 AGGCTGTAAGGATTACTTAGTTCTCCCTTATTAGGAAACTCTTTTCTCTGTGGAGTTAGCA 299

Qy  3731 gcacaagggcaaatcccgttccttcaacggaaaaaacattcctaaggtaaagaa 3790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 GCACAAGGGCAAATCCCGTTTCTTTAACAGGAAGAAGAACATTCCTAAGGTAAAGAA 359

Qy  3791 cagattcaagccctagtcttgctgactaatatgatggttctttttgaaaaatcaattcagcg 3850
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 CAGATTCAAGCCCTAGGTCTTGCTGACTAATATGATTGGTTTTTTGAAAAAATCAATTCAGCG 419

Qy  3851 atgtttactatctgattcaggaaaatgagaactagtacccctttggtcagctgataaacaaaca 3910
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3851 ...
```

```
Qy  4261 tgttttttaccacccttctaactaaattaacacttattccaattgcgaatagagccaataa 4320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  4261 TGTTTTTTACCACCCTTCTAACTAAATTTAACACTTATTCCAATTGCGAATAGAGCCATAA 4320

Qy  4321 ctcaaagtggtaataaccagtacctgtgatttgtcattaccaataagaaatcacagacatt 4380
         |||||||||||||||||| |||||||||||||||||||||||||| |||||||||||||||
Db  4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy  4381 ttatactatattacagttgttgcagatacgttgtaagtgaaatatttatacttcaaaacta 4440
         |||||||||||||| |||||||||||||||||||||||||||||||||||||| |||||||
Db  4381 TTATACTATATTACACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

Qy  4441 ctttgaaattagacctcctgctcttgttcttaacatataataaaacatgtttaaa 4500
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  4441 CTTTGAAATTAGACCTCCTGCTCTGTTTTTTAACATATAATAAAACATGTTTAAA 4500

Qy  4501 atttgatatttgataatcattatattcattatcattgttccttgtcaatctatatattt 4560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501 ATTTTGATATTTGATAATCATTATATTTCATTATCATTTGTTTCCTTGTGTAATCTATATTTT 4560

Qy  4561 atatattcgaaaacaatcttctcggaagaagtttcccccagatttccccaatgagggttcttgg 4620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561 ATATATTTGAAAACATCTTTCTCGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy  4621 catgcacacacacacaagtaagaactgattttaggagggtaacaatggactggctgctaaga 4680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621 CATGCACACACACAGAGTAAGAACTGATTTTAGGGTAACTGGACTGGTGGCTGGCTAAGA 4680

Qy  4681 tgcaagactgaaattagaaagttctctccaaagatcacacacagtcttgttgtttaaagctt 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681 TGCAAGACTGAAATTAGAAAGTTCTCTCCAAAGATACACACAGTTGTTTTAAAGCTTAGGGGTG 4740

Qy  4741 agggggggaaatctgcgcgtctctatagggatgtctctccctggagcctggtaggttgc 4800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4741 AGGGGGGAAATCTCGCGCTTCTAGAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGGCTGTGTC 4800

Qy  4801 cttgtgttctggctggcgtcgttatttttctcgtcctgctcttcttaaaggactgttt 4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801 CTTGTGTTCTGGCTGGCGTCGTTATTTTTCTCGTCCTGCTCTTAAAGGACTTGTTT 4860

Qy  4861 ggatctccagttcctagcatagtgccctgccacagtgcaggttccaatgaagttgcacag 4920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861 GGATCTCCAGTTCCTAGCATAGTGCCTGCCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy  4921 tgaatgggaaatataaactagaaaatatatatccctttgttgaaatcagcacacacagtagtcctgg 4980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921 TGAATGGGAAATATAAACTAGAAAATATATCCTTGTTGAAATCAGCACACACAGTAGTCCTG 4980

Qy  4981 tgtaagtgtgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgaaaacaggtgggagta 5040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTAAAATCAGGTGTGTGTAAAACAGGTGGGAGATA 5040

Qy  5041 taggaactattattgggtatgggtgcataaatgttgcataaaattgggatgtcttcttaaaaagaaaactc 5100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041 TAGGAACTATTATTGGGTATGGGTGCATAAATGTTCTTTTGTGTCATAAAATTGGGATGTCTTTTTTAAAAAGAAAACTC 5100

Qy  5101 caaacagacttctggaaggttatttattttcttaagaatctttgctcgagctggaagcaacccc 5160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101 CAAACAGACTTCTGGAAGGTTATTTATTTTCTTAAGAATCTTTGCTCGAGCTGGAAGGCAAACCCC 5160

Qy  5161 cctgtgtgacagccgcccaccccagccctgtcttctccccatgaaggctg 5220
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5161 CCTGTGTGACAGCCGCCCACCTCTGTCTTCTCCCCATGAAGGGCTG 5220

Qy  5221 gctccccagtatatataaacctctctggagctcgggcatgaagccagcaagccacccatc 5280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5221 GCTCCCCAGTATATATAAACCTCTCTGAGCTCGGGCCATGAAGCCAGCAAGGCCACCCATC 5280

Qy  5281 caggcaacctcctcagcacagc 5300
         ||||||||||||||||||||||
Db  5281 CAGGCAACCTCTCAGCACAGC 5300
```

```
Db    420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGGTCAGCTGTAAACAAACA 479
Qy   3911 cccagCttgtaaatgtcctcaagtcaggcttaactgcagaaccaaatcaaa-aagaataga 3969
Db    480 CCCATTGTAAATGTCTCAAGCTTAACTGCAGAACCAAATCAAATAAGAATAGAA 539
Qy   3970 tcttagaggagaaactgtgtttcctcacatctggggtggactgcagaagggagttga 4029
Db    540 TCTTTAGAGCAGAAACTGTGTTTCTCCAC--TCTGGAGGTGGAGGTCAGCTGCAGAGTTGGAA 598
Qy   4030 atattacttcacacagtatctgacacgtattggttattacacacataaagttgctcaaag 4089
Db    599 ATATTTACTTCACACAGTATTGACACTGTTGTTGGGATTATAACAACATAAAGTTGCTCAAAG 658
Qy   4090 gcaatcaatcatttattggttctaagttacctctgacagttttggtatattttattggct 4149
Db    659 GCAATCAATTATTTCACAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTTATTGGCT 718
Qy   4150 attgccaattgcttttgtttttgtttttcctttgggtttattattaaagcaggga 4209
Db    719 AATTGCCAATTTGCTTTTGTTTTTGTTTTTCTCCTTTGGGGTTTATTATTAAAGCAGGGATATTA 778
Qy   4210 acctacagtccagaaagcctgtgaatttgaatttgaatgaggaaaaattcaatttgtctttac 4269
Db    779 ACCTACAGTCAGAAAGCCTGTGAATTTGAATGAGGAGGAAAAATTACATTTTTGTTTTTAC 838
Qy   4270 cacctctaaactaaaatttaacactttattctccatggctaaagttctttettetetggct 4329
Db    839 CACCTTCTAACTAAAATTTAACAGTTTTACTTCTGACAGTTTGTATATTTTATTGGCT 898
Qy   4330 gtaataaacagtaccctgtgaatttgacattttgtcattttttatactat 4389
Db    899 GTAATAAACAGTACCCTGTGAATTTGCATTACCAATAGAAAATCACAGACATTTTAATACTAT 958
Qy   4390 attacagttctgtgcaataccgttgtaagtgaaatatttactctcaaaactacttaaat 4449
Db    959 ATTACAGTTGTTGCAGATACCGTTGTAAGTGAAATATTTTATACTCAAAACTACTTGAAAT 1018
Qy   4450 tagacctcctggatctgttgttttatagacatttaatcatattatatttg 4509
Db   1019 TAGACCTCCTCGGATCTGTTTTTATAACATTTAATACTTATTTATAAACTTTATACTTT 1078
Qy   4510 ttttgatataacaatattcattacattgttccttttgtaaatctatattttatatatttg 4569
Db   1079 TTTTGATAATATTCATTATATTTGTTTCCTTTGTAATCTATATATTTATATAATTTG 1138
Qy   4570 aaaacatctcttctgtgaaagagttcccagatgtttcaccagtcttggcatgcacac 4629
Db   1139 AAAACATCTTTCTGTGAGAAGAGTTCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198
Qy   4630 acacagagtaagaactgattagggctaacattggtgcctgagaatgcaagact 4689
Db   1199 ACACAGGTAAGAACTGATTTAGAGGCTAACATTGGTGCCTGAGAATGCAAGACT 1258
Qy   4690 gaaatagaaagttctcccaagatacacagtacttggtctaaggctaggggggggaa 4749
Db   1259 GAAATAGAAAGTTCTCCAAAGATACAACAGTTGTTTAAAGCTAGGGTGAGGGGGAA 1318
Qy   4750 atctgccgcttctatagggatgctctccccctggtctggtctgctgtcctctgtgttc 4809
Db   1319 ATCTCGCCGCTTCTATAGGAAATGGCTCTCCCTGGTATGGGTGCTGTGCCTTGTTC 1378
Qy   4810 tggctggctgttatttgttattggttttgggatcctca 4869
Db   1379 TGGCTGGCTGTTATTTTCTCTGTCCCTGCCTTAAAGGACTTGTTTGGATCTCCA 1438
Qy   4870 gttcctagtcatagtccctcgcacagttctcaatgagtgttatggaa 4929
Db   1439 GTTCCTAGCATAGTGCCTGGCAAGTTTCAGCAGGTCGATAATGGCTCTACAGGCG 1498
Qy   4930 atataaactaggaaaatatatcctttgtttgaaatcagcaccacccagtagtcctctggtgtaagtgt 4989
Db   1499 ATATAAACTAGAAAATATCCTTGTTTGAAATCAGCACCACCACCAGTAGTCCTGTCTGTAAGTGT 1558
```

```
Qy   4990 gtgtacgtgtgtgtgtgtgtgtgtgtaaaacaggtggagaatataggaacta 5049
Db   1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTAAAAACCAGGTGAGATAAGGAACTA 1618
Qy   5050 ttattgggttatggtgcataaactgggatgttcttttaaaaagaaaacctccaaacgac 5109
Db   1619 TTATTGGGGTATGGGTGCATAAATGTGGATGGTTCTTTTTTTAAAAGAAAACTCAAACAGAC 1678
Qy   5110 ttcttgaaggttattttctaagaaatcttgctctgggcacgtgaaggcaaccctgtgcac 5169
Db   1679 TTCTTGGAAGGTTTATTTTCTAAGGAAATCTTGCTCTGGGCACGTGGAAGGCAACCCCTGTGCAC 1738
Qy   5170 agcccaccccacctcacgtggccaccctctgtcttccccccatctgaaggggtcccag 5229
Db   1739 AGCCCACCCCAGCCTCACGTGGCCACCCTCTGTCTTCCCCCCATCTGAAGGGGGTCCCCAG 1798
Qy   5230 tatatataaacctctctgagagtccagtagccagctcggggcatgggaccctca 5289
Db   1799 TATATAAAACCTCTCTGGAGCTGGCCACCTCGTCTTCCCCCATGGGGGACCCATCT 1858
Qy   5290 ctcagcacagcagagagtcttcagaagacctcacaagcaagcctctgcaatgaggttctct 5349
Db   1859 CTCAGCACAGCAGAGAGCTTTCAGAAGACCTCACAAGCAAGCCTCTGCAATGAGGTTCTCT 1918
Qy   5350 gtgcacgttgtgcagcttcgccagtcagctgtgctgcct 5409
Db   1919 GTGCACGTTGTGCAGCTTTGGGCCTGAGAATGCCAGTGCCAGCTGCTGTTCTGCCT 1978
Qy   5410 gcctgtgttgggagtgtggggggcatgggggccagatgtcagcctcactaacttacacgac 5469
Db   1979 GCCTGGTGCTGGGAGTGTGGGATGGGGGCCAGGCTCAGCTCACTAACTTACAGCAACTTACCTTAT 2038
Qy   5470 gccggatgccagtataccttgggtggccaagctccctggaagtccctggagagagaga 5529
Db   2039 GCCGGATGCCAGTATACCTTCAGTGTGGCGGCCAAGCTCCCTGGAAGTCCCTGGAGAGAGAGA 2098
Qy   5530 gccaggccagtcatcagtcatcatcataacttacagctcagctcctttagac 5589
Db   2099 GCCAGGGCCACCAAAGCTGACTTCAGCTCCAGCACAGGCCTCTGCACACAGCCAGAGTG 2158
Qy   5590 tgggagggccacacaaagctcgctctccctcctcaccaccaccccaacggcttgacc 5649
Db   2159 TGGGAGGGCCACACAAAGCTCGCTCTCCTCCTCCACCACCAACTTGACCTTGG 2218
Qy   5650 accaggggctcaaggctgcaggaccacccagtcagcaggagagggggggcaccctga 5709
Db   2219 ACCAGGCTGCCAGGCCCCCAGAGAGCCCCAGGCAGGAGGGGTGCGCAGGGCACCCTGA 2278
Qy   5710 ggcgggaggcgggaccagctgggaaaaaccaacaggagtcggagactacagacc 5769
Db   2279 GGCGGGAGGCGGGGACCAGCTGGGAAACCCAAAACCAGAGAGTGCCTACAGCAAACC 2338
Qy   5770 tcctccgagacaagtcagttctgagggaagagagaagcgcactagggaaaaatgaga 5829
Db   2339 TCCTCCGAGACAAGTCAGTTCTGGAGGAAGAGAGAAGCGCACTAGGGAAAAATGAGA 2398
Qy   5830 atctgggcagagaggttggaaagcaagcagagcaggagaggaggagggggccagt 5889
Db   2399 ATCTGGGCCAGAGAGGTTGGAAAGCCAGCAGAGCAGGAGAGGAGGGGGGCCAGT 2458
Qy   5890 gtcccagagaccctcggggctccagaggctccagaggagagttaagaggggtaagatg 5949
Db   2459 GTCCCAGAGACCCGCAGGGCTCCGGGCGTCCCACCAGGGAGATAAGGCTCCAGAGAATG 2518
Qy   5950 cagagtggggggacttcagcaggtgaatatggggggctgtagtccggctgctacaggcg 6009
Db   2519 CAGAGTGGGGGGGGACTTCAGCAGGTCGATAATGGCTCGGGTTAGTCGACCTGCTACAGGCG 2578
Qy   6010 ctccaggccctc-----ctgcctttctcctagagacttgcacagctagcacagacagtg 6065
Db   2579 CTCCAGGCCCTCGGCTGCCCTTTCTCCTAGGGACTGCAAGCTAGCCACCAAGACAGATG 2638
```

```
Qy     6066 aattaaggaaagcaca-cgatcacacctccaagtatattctggacctcctgaaagct 6124
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     2639 AATTAAGGAAAGCACACAGATCACACCTTCAAGTATTACTAGTAATTTAGCTCCTGAGAGCT 2698

Qy     6125 tcatttagattagtcggttcaagtttccttgtgccctccccatgtcag 6169
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     2699 TCATTTAGATTAGTCGGTTCAAGTTTCTTGTGTCCCCTCCCATGTCAG 2743
```

```
                                   exon            431..1077
                                                   /number=1
                                                   /product="myocilin"

               BASE COUNT      312 a      325 c      350 g      241 t
               ORIGIN

Query Match          19.3%;  Score 1190.4;  DB 9;  Length 1228;
Best Local Similarity 99.4%;  Pred. No. 1.4e-249;
Matches 1217;  Conservative  0;  Mismatches  1;  Indels  6;  Gaps 2;
```

```
Qy     4862 gatctccagttcctagcatagtgcctggacaagtgcaggttcctccaatgagtgccagagt 4921
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GATCTCCAGTTCCTAGCATAGTGCCTGGACAAGTGCAGGTTCCTCCAATGAGTTTGCAGAGT 60

Qy     4922 gaatggaaatataaactagaaaataatatatccttgttgaaatcagcacaccagtagtccggt 4981
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GAATGGAAAATATAAACTAGAAAATAATATATCCTTGTTGAAATCAGCACACCAGTGTCCTGGT 120

Qy     5102 aaacagacttctggaaggttatttctaagaatcttgcttggctgtgtgtgggcaaccccc 5161
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      239 AAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTTGCTTGGCTGTGTGTGGGCAACCCC 298

Qy     5042 aggaactatatttgggtatgggttgcataaattgggagtgtctcttttaaaagaaactcc 5101
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      179 AGGAACTATTATTTGGGGTATTGGGTGCATAAAATTGGGAGTGTTCTTTTTAAAAAGAAACTCC 238

Qy     4982 gtaagtgtcgttacgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagat 5041
            ||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db      121 GTAAGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGTGTGTGTAAAAACCAGGTGGAGATAT 178

Qy     5162 ctgtgcacagcccaccccagcctcacgtggccaccctctgtctcccccatgaagggctgg 5221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      299 CTGTGCACAGCCCACCCCAGCCTCACGTGGCCACCTCTGTCTCCCCCATGAAGGGCTGG 358

Qy     5222 ctccccagtatatataaacctctctggagctcgggacttgagccagcaaggccaccatcc 5281
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      359 CTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGACTCGAGCCAGCAAGGCCACCATCC 418

Qy     5282 aggcacctcacacacagacgtttccaggaggaggaagcctcaccacagcctctgaatgag 5341
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      419 AGGCACCTCACACACAGACGTTTCCAGGAGGAGGAAGCCTCACCACAGCCTCTGCAATGAG 478

Qy     5342 gttcttctgtgcacgttgctgcagcttgggccctgagagtgccagctgtccagctgctct 5401
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      479 GTTCTTCTGTGCACGTTGCTGCAGCTTGGGCCCTGAGATGCCAGCTGTCCAGCTGCTGCT 538

Qy     5402 tctggcctgcctggttgttgggatgtggggccagagcagctcagcgaggaaggccaatga 5461
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      539 TCTGGCCTGCCTCCCTGGTGTTGGGATGTGGGGCCAGAGCAGCTCAGCGGAAGGCCAATGA 598

Qy     5462 ccgagagtggccagtgtataccttcagtgtggggccagtccaaatgaatccgagctgccc 5521
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      599 CCGAGAGTGGCCGGATCCCAGTGTATACCTTCAGTGTGGGGCCAGTCCAAATGAATCCGAGCTGCCC 658

Qy     5522 agagcagagccaggcccatgtcagtcatccataacttacagagagacagcagcaccacacg 5581
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      659 AGAGCAGAGCCAGGCCCATGTCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAACG 718

Qy     5582 cttagacctgaggcacacaaagctcgactcagctcagctctggaggcctcctccaccaatt 5641
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      719 CTTAGACCTGGAGGCCACCAAAGCTCGACTCAGCTCCCTGGAGGCCTCCTCCACCAATT 778

Qy     5642 gacttgaccctggcagggccccaggaaccgggaagggggggctgcaggggaagctggg 5701
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      779 GACCTTGGACCAGGCCTGCCAGGGGGACCCCAGGAAGGGGGGGCTGCAGGGGAAGCTGGG 838

Qy     5702 caccctgagcgcgggacgcgggaccaagctgaaacccaaacccagaggagtctggagagctgccta 5761
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      839 CACCCTGAGCGCGGGGAGCGGGACCAGCTGAAACCAAAACCCAGAGAGTTGGAGACTGCCTA 898

Qy     5762 cagcaacctccctccgagacaagtcagttctggaggaagaaggagcgactaaggcaaga 5821
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT   6
LOCUS       HSGLC1A1          1086 bp     DNA             PRI       30-JAN-1998
DEFINITION  Homo sapiens GLC1A (trabecular meshwork induced glucocorticoid
            response) gene, exon I, joined CDS.
ACCESSION   Z97171
VERSION     Z97171.1     GI:2425156
KEYWORDS    GLC1A.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1086)
AUTHORS     Stone,E.M., Fingert,J.H., Alward,W.L., Nguyen,T.D., Polansky,J.R.,
            Sunden,S.L., Nishimura,D., Clark,A.F., Nystuen,A., Nichols,B.E.,
            Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C.
TITLE       Identification of a gene that causes primary open angle glaucoma
JOURNAL     Science 275 (5300), 668-670 (1997)
MEDLINE     97158493
REFERENCE   2  (bases 1 to 1086)
AUTHORS     Adam,M.F., Belmouden,A., Binisti,P., Brezin,A.P., Valtot,F.,
            Bechetoille,A., Dascotte,J.C., Copin,B., Gomez,L., Chaventre,A.,
            Bach,J.F. and Garchon,H.J.
TITLE       Recurrent mutations in a single exon encoding the evolutionarily
            conserved olfactomedin-homology domain of TIGR in familial
            open-angle glaucoma
JOURNAL     Hum. Mol. Genet. 6 (12), 2091-2097 (1997)
MEDLINE     97472461
REFERENCE   3  (bases 1 to 1086)
AUTHORS     Garchon,H.J.
TITLE       Direct Submission
JOURNAL     Submitted (20-JUN-1997) Garchon H.-J., Hopital Necker, INSERM U25,
            161 rue de Sevres 75743 Paris cedex 15 FRANCE
FEATURES             Location/Qualifiers
     source          1..1086
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="q23-q25"
                     /tissue_type="white blood cells"
     TATA_signal     35..363
     exon            385..1065
                     /gene="GLC1A"
                     /label=ex1
                     /number=1
     mRNA            join(385..1065,297177.1:21..146,297174.1:21..1475)
                     /gene="GLC1A"
                     /label=NAGLA1A
     gene            join(385..1065,297177.1:21..146,297174.1:21..1475)
                     /gene="GLC1A"
     misc_feature    462..1065
                     /gene="GLC1A"
                     /note="first coding exon"
                     /label=start
     CDS             join(462..1065,297177.1:21..146,297174.1:21..805)
                     /gene="GLC1A"
                     /codon_start=1
                     /label=CDSGLC1A
                     /protein_id="CAB09999.1"
                     /db_xref="GI:2425157"
                     /db_xref="SWISS-PROT:Q99972"
                     /translation="MRFFCARCCSFGPEMPAVQLLLACLVWDVGARTAQLRKANDQS
                     GRCQYTFSVASPNESSSCPEQSQAMSVIHNLQRDSSTQRLDLEATKARLSSLESLLHQL
                     TLDQAARPQETQEGQRELGTLRRERDLETQTRELETAYSNLRDKSVLEEEKRLR
                     QENENLARRLESSSQEVARLRRGQCPQTRDTARAVPPGSSREVSTWNLDPLAFQELKSE
                     LTEVPASRILKESPSGYLRSGEGDTGCGELVWVGEPLTLRTAEETIGKYGVWMRDPKP
                     TYPYTQETTWRIDTVGTDVRQVFEYDLISQFMQGYPSKVHILPRRLESTGAVVYSGSL
                     YFQGAESRVIRYELNTETVKAEREIPGAGYHGQFPYSWGGYTDIDLAVDEAGLMVIY
                     STDEAKGAIVLSKLNPENLELEQQTWETNIRKQSVANAFIICGTLYTVSSYTSADATVN
                     FAYDTGTGISKTLTIPFKNRYKYSSMIDYNPLEKKLFAWDNLNMVTYDIKLSKM"
BASE COUNT      277 a    282 c    316 g    211 t
ORIGIN
```

Query Match   17.68;   Score 1084.4; DB 66;   Length 1086;
Best Local Similarity   99.9%;
Matches 1085; Conservative   0; Mismatches 1; Indels   0; Gaps   0;

```
Qy  4876 agcatagtgcctgctgagcatgtgcaggttctcaataatgagtttcgagagtgaatgaaataataa 4935
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGCATAGTGCCTGCTGAGCATGTGCAGGTTCTCAATAATGAGTTTCGAGAGTGAATGAAAATATAA 60

Qy  4936 actagaaatatatcccttgtgaaatcagcagcaccaccagtagtcctggtgtgtaagtgtgtgtac 4995
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ACTAGAAATATATCCCTTGTGAAATCAGCACACACCACCAGTAGTCCTGGTGTGTAAGTGTGTGTAC 120

Qy  4996 gtgtgtgtgtgtgtgtgtgtgtgtgtgtaaaacccaggtggagaataaggaaactattattg 5055
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCACACCAGTAGGAGAATAGGAACACTATTATTG 180

Qy  5056 ggggtatgggtgtgcataaattcggggatgtgttctttctttaaaagagaaactccaaaacagactttctgg 5115
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGGTATGGGTGTGCATAAAATTGGGATGTTTCTTTTAAAAGAGAAAATCCAAAACAGACTTCTGG 240

Qy  5116 aaggttatttctaagaaatctcttggcagcgtgaaggcaccacccctgtgcacagcccc 5175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGGTTATTTTCTAAGAAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTCCACAGCCCC 300

Qy  5176 acccagcctcacgtggccacctcgttcttccccccatgaaggctggctccccagtatata 5235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACCCAGCCTCACGTGGCCACCTCGTTCTTCCCCCCATGAAGGGCTGGCTCCCCAGTATATA 360

Qy  5236 taaacctctctggagctcgggcatgaagcccaagccccatgaaggtttcttcttgtgcac 5295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TAAACCTCTCTGGAGCTCGGGCATGAAGCCCAAGGCCCATCAGCACCCTCAGC 420

Qy  5296 acagcagagagctttcgggagctcggctcaccaaggcctctgcacaagcctcacactgcac 5355
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ACAGCAGAGAGCTTTCCACGAGGAAGCCCTCACCAAGGCCTCTGCACAAGCCTCAC 480

Qy  5356 gttgctgcagcttgggcctgagatgccagtccagctgctgcttctggcctgg 5415
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTTGCTGCAGCTTTGGGCCTGAGATGCCAGTCCAGCTGCTGCTTCTGGCCTGG 540

Qy  5416 tgtgggatgtggggcccaggagacagctcagctcaggagggccaatgaccaagagttggccgat 5475
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGTGGGATGTGGGGCCCAGGAGACAGCTCAGCTCAGGAGGGCCAATGACCACAGTGCCGGCGAT 600

Qy  5476 gccagtataccttcagtgtggccagtcccaatgaatccagctgccaagagcagagagcagg 5535
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTGCCCAGAGCAGAGCCAGG 660

Qy  5536 ccaatgtcagtcatccataacctacagagagacgcagcaccaacgcttagacctggagg 5595
```

Db   899 CACCAACCTCCTCCGAGACAAGTCAGTTCTCTGGAGGAAGAAGAAGCGACTAAGGACAAGA 958
Qy 5822 aaatgagaatctggccaggagggttggaaagcagcagccaaggctgagaag 5881
Db   959 AAAATGAGAAATCTGGCCAGGAGGGTTGGAAAGCAGCAGGGAGGCTGAGAAG 1018
Qy 5882 gggccagtcgtgtcccagaccagcaacactgctcggggctcgggcgctccaagagaagg 5941
Db 1019 GGGGCAGTCGTCCCCAGACCAGCAACACTGCTCGGGGCTGTTCCCACCAGGAGAAGG 1078
Qy 5942 taaggaaatcagtgggggggacttctgagtgtcagtctcctagtca 6001
Db 1079 TAACGAAATCAGCAGTGGGGGGGACTGTGAGTTCAGGAGTGATATGGCTCTCGTTAGGTGACCTGC 1138
Qy 6002 taccaggcgctccaggcctc----cctgcccttcctcctaggagagactgccacagtctagacaca 6057
Db 1139 TACAGGCGCCTCCAGGCCTCCTCCGTGCCTGCCTTTCTCCTAGAGACTGCCACAGCTAGACACA 1198
Qy 6058 gacaggagaggaattaaggaaagcaca 6081
Db 1199 GACAGAGATGAATTAAGGAAAGCACA 1222

```
RESULT 7

LOCUS       D88214      1934 bp    mRNA           PRI       07-FEB-1999
DEFINITION  Homo sapiens mRNA for myocilin, complete cds.
ACCESSION   D88214
VERSION     D88214.1  GI:2627176
KEYWORDS    myocilin.
SOURCE      Homo sapiens retina cDNA to mRNA, clone_lib:human retina cDNA
            library 5'stretch (CONTECH).
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1934)
AUTHORS     Shimizu,N.
TITLE       Direct Submission
JOURNAL     Submitted (02-OCT-1996) to the DDBJ/EMBL/GenBank databases.
            Nobuyoshi Shimizu, Keio University School of Medicine, Department
            of Molecular Biology; 35 Shinanomachi, Shinjuku-ku Tokyo 160,
            Japan (E-mail:shimizu@dmb.med.keio.ac.jp, Tel.03-3351-2370,
            Fax:03-3351-2370)
REFERENCE   2  (sites)
AUTHORS     Kubota,R., Noda,S., Wang,Y., Minoshima,S., Asakawa,S., Kudoh,J.,
            Mashima,Y., Oguchi,Y. and Shimizu,N.
TITLE       A novel myosin-like protein (myocilin) expressed in the connecting
            cilium of the photoreceptor: molecular cloning, tissue expression,
            and chromosomal mapping
JOURNAL     Genomics 41 (3), 360-369 (1997)
MEDLINE     97312692
COMMENT     On Nov 20, 1997 this sequence version replaced gi:2104213.
            Sequence updated (17-Nov-1997).
FEATURES             Location/Qualifiers
     source          1..1934
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q23-q24"
                     /clone_lib="human retina cDNA library 5'stretch (CONTECH)"
                     /tissue_type="retina"
     CDS             65..1579
                     /codon_start=1
                     /product="myocilin"
                     /protein_id="BAA23531.1"
                     /db_xref="GI:2627177"
                     /translation="MRFCARCCSFGPEMPAVQLLLACLVWDVGARTAQLRKANDQS
                     GRCQYTFSVASPNESSCPEQSQAMSVHLQRDSSTQRLDLEATKARLSSLSLLHQL
                     QENENLARRLESSSQEVARLRRQCPQTRDTARAVPPGSREVSTWNLDTLAFQELKSE
                     TLEVPARRILKPSPSGYLRSGEDLDVRQYEEYDDISQFMQGYPSKVHLPPFLSTG
                     TYPYTQETTWRIDTVGTDVRQYEEYDDISQFMQGYPSKVHLPPFLSTGAVVYSGSL
                     YFQGAESRVIRYELNTETTVKAEKEIPGAGYHGQFPYSWGGYTDIDLAVDEAGLWVIY
                     STDEAKAIVLKLNPENLELEQTWETNIRKQSVANAFIICGTLYTVSSYTSADATVN
                     FAYDTGTGISKILTIIPKNRYKYSSMIDYNPLEKKLFAWDNLNMVTYDIKLSKM"
     old_sequence    104..105
                     /citation=[2]
                     /replace="gaga"
     misc_feature    317..361
                     /note="leucine zipper-like motif 1"
     misc_feature    413..562
                     /note="leucine zipper-like motif 2"
     polyA_signal    1778..1783
     polyA_signal    1928..1933
BASE COUNT      510 a    503 c    525 g    396 t
ORIGIN

Qy   5287 cctctcagcacagcagagcgttccagaggaaagatgccagctgtccagctgctcctctgg 5406
          |||| ||                                              || |||||
Db     15 CCCCTCTCCACAGCAGAGACGTTTTCCAGAGGAAAGCTTCACCAAGCTTCTCCAAATGAGGTTCT 74

Qy   5347 tctgtgcacgttgctgcagctttgggcctgaggatgccagctgctgttctgg 5406
          ||| |||   ||||||||||||||||||| |||||||||||||| || ||||
Db     75 TCTGTGCACGTTGCTGCACTTTGGGCCTGAGGATGCCAGCTGCTGTTCTGG 134

Qy   5407 cctgcctggttgtgtggggattgggggggccaggagaccaagctcaggagaccga 5466
          ||| ||||||||||||||||||| ||||| ||||||| ||||| ||||||| ||
Db    135 CCTGCCTGGTTGTGTGGGGATTGGGGGGGCCAGGACAGCTCAGGTCAGGAGACCAGA 194

Qy   5467 gtggccgatgccagtatacctcagtgtcggccagtcccaatgaatccagctgccagagc 5526
          ||||||     ||||||||||||||||| |||||||||||||||||| |||||||||||
Db    195 GTGGCCGATGCCAGTATACCTTCAGTGTGTGGCCAGTCCCAATGAATCCAGCTGCCAGAGC 254

Qy   5527 agagccaggccatgtcagtcatccataacttacagagagacagcagcacccaacgcttag 5586
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    255 AGAGCCAGGCCATGTCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAACGCTTAG 314

Qy   5587 aacctggaggcacacaaagctcgactcagctcctggagagccctccaccattgacct 5646
          ||||||||||| |||||||||||||||| ||||||||||||||||||||| ||||||
Db    315 ACCTGGAGGCGCACCAAAGCTCGACTCAGCTCCTGGAGAGCCCTCCACCAATTGACCT 374

Qy   5647 tggaccaggctgccaggcgcccagagaggaagaaagaaccactaggcaggagaaatg 5706
          ||||||||||||||||| ||||||||| ||||||||||||| ||| ||||||||||
Db    375 TGGACCAGGCTGCCAGGCCCCCAGGAGAGACCCAGGGGGCGTGCAGGGGAGCTGGGCACC 434

Qy   5707 tgaggcgggaggggaccaagctggaaaacccaaaccagagaggcttggagactgcctcagca 5766
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||| ||||||
Db    435 TGAGGCGGGAGGGGACCAGCTGGAAAACCCAAACCAGAGAGGCTTGGAGACTGCCTCAGCA 494

Qy   5767 acctcctccgagacaaagtcatgctctgggtgggaggaaagaaagcaactagggcaggagat 5826
          |||||||||||||||||||| ||||||||||||||||| |||||||||||||||||| ||
Db    495 ACCTCCTCCGAGACAAAGTCGTGCACAAGTCAGTTCTTGGAGGAAGAAGCGACTAAGGCAGGAAATG 554

Qy   5827 agaatctggccaggagagttggaaagcagcagccagccaggaggtagcaaggctgagaaggggcc 5886
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    555 AGAATCTGGCCAGGAGAGGTTGGAAAGCAGCAGCCAGCCAGGAGGTAGCAAGGCAGAAGGGGC 614

Qy   5887 agtgtcccagacccggagacactgctcgggctgtgtcccacccaggctccagagagaaggt 5942
          |||||||||||||| ||||||||||| ||| ||||||||||||||||||||||||||| |
Db    615 AGTGTCCCCAGACCCGGAGACACTGCTCGGGCTGTGTCCCACCCAGGCTCCAGAGAAGAGTT 670

Qy    661 CCATGTCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAAAGCGTTAGACCTGGAGG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCACCAAAGCTCGACTCAGCTCCTCCTGGAGAGCCCTCCACCAATTGACCTTGGACCAGG 780

Qy   5596 ccacaaaagtcctgactccctggggagaggacccctctccaccaatttgaccttggaccagg 5655
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCACCAAAGCTCGACTCAGCTCCTCCTGGAGAGCCCTCCACCAATTGACCTTGGACCAGG 780

Qy   5656 ctgccaggcgcccagagaggacccctcaggagggaggaggtcctgccacctcgggggggg 5715
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGCCAGGCCCCCAGAGGCCCCAGGAGGGGCTGCAGGGGAGCTGGGCACCTGAGGCGGG 840

Qy   5716 agcgggaccagctgggaaaacccaaaccagagaggactgcctacagcaacctcctcc 5775
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AGCGGGACCAGCTGGGAAAACCCAAAACCAGAGAGGACTCCCTAGCAGCAACCTCCTCC 900

Qy   5776 gagacaagtcagttctgggagggaggaagaagcgactaaggcaaggaaaatgagaaatctgg 5835
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    901 GAGACAAGTCACTTCTGAGGAAGAGAAGCGACTAAGGCAAGAAAAATGAGAAATCTGG 960

Qy    901 ccaggaagttggaagacaagcagccaaggctgagcaagctggccagtgtcccc 960

Qy   5836 ccaggaagttggaagcagcagccaggctgcaggggcaggtgtcccc 5895
          |||||||||||||||| ||||||||||||| |||||||||||||||
Db    961 CCAGGAAGTTGGAAAGCAGCAGCCCGAGGAGGTGGGCACCTGAGGCGGG 1020

Qy   5896 agaaccgagacactgctccgggctgtgtccccaccaggatgaagtgtaagaatgcaggt 5955
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGACCCGAGACACTGCTCCGGGCTGTGTCCCCACCCAGGCTCCAGAGAAGGTAAGAATGCAGAGT 1080

Qy   5956 ggggg 5961

Db   1081 GGGGG 1086
```

Query Match   10.6%;   Score 651.2;   DB 35;   Length 1934;
Best Local Similarity 99.5%;
Matches 653;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Pred. No. 5.4e-132;

RESULT 8

LOCUS   AR030962   1999 bp   DNA   PAT   29-SEP-1999
DEFINITION   Sequence 2 from patent US 5861497.
ACCESSION   AR030962
VERSION   AR030962.1 GI:5944176
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 1999)
  AUTHORS   Nguyen,T.D., Polansky,J.R. and Huang,W.
  TITLE   Trabecular meshwork induced glucocorticoid response (TIGR) nucleic
                acid molecules
  JOURNAL   Patent: US 5861497-A 2 19-JAN-1999;
FEATURES   Location/Qualifiers
     source   1..1999
                     /organism="unknown"
BASE COUNT   537 a   508 c   534 g   420 t
ORIGIN

Query Match   10.4%; Score 640.4; DB 5; Length 1999;
Best Local Similarity   99.8%; Pred. No. 1.2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   5301 agagcttccagaggaggaagcctcaccaagcctctgcaatgaggttcttctgtgcacgttgc 5360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGAGCTTTCCAGAGGAGGAAGCCTCACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60

Qy   5361 tgcagcttgggcctgagatgccagctgccagctgcttctgtctggcctgtctcctgtgtgg 5420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCAGCTTTGGGCCTGAGATGCCAGCTGCCAGCTGCTTCTGGCCTGTCTCCTGTGTGG 120

Qy   5421 gatgtggggggccaggacagctcagctcaggagaaggccaatgaccagagtgccgatgccag 5480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGAGAAGGCCAATGACCAGAGTGCCGATGCCAG 180

Qy   5481 tataccttcagtgtggccagtcccaatgaatccagcgtgcccagaagcagcaggccagccatg 5540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCGTGCCCAGAAGCAGCAGGCCAGCCATG 240

Qy   5541 tcagtcatccataacttacagagagacttagacctggagactgagccacc 5600
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAGTCATCCATAACTTACAGAGAGACTTAGACCTGGAGACTGAGCCACC 300

Qy   5601 aaagtccgactcagctccctggagagagcctccctccaccacaattgacccttggaccaggctgcc 5660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAAGCTCGACTCAGCTCCCTGGAGAGAGCCTCCCTCCACCACAATTGACCCTTGGACCAGGCTGCC 360

Qy   5661 aggccccaggagagacccaggaggggggcctgggcacccctgaggcggcggggagcgg 5720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGGCCCCAGGAGAGACCCAGGAGGGGGGCCTGGGCACCCCTGAGGCGGCGGGGAGCGG 420

Qy   5721 gaccagctggaaaacccaaaccagagggactgctactacagacaactcctccgagac 5780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGCTGGAAAACCCAAACCAGAGTTGGAGACTGCTACAGACAACTCCTCCGAGAC 480

Qy   5781 aagtcagttctctggaggaggaagacgaactaaggccaggaaatctggccagg 5840
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAGTCAGTTCTCTGGAGGAGGAAGACGACTAAGGCAAGAAAATGAGAATCTGGCCAGG 540

Qy   5841 aggttggaaagcagcagcccaggatagccagaggcttgagtgtcccagacc 5900
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGGTTGGAAAGCAGCAGCCCAGGAGGTAGCAAGGCTTGAGGAAGGGCCAGTGTCCCAGACC 600

Qy   5901 cgagacaactgctcgggctgtgtgccaccaggctctcccagaggaaggt 5942
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CGAGACACTGCTCGGGGCTGTGCCACCAGGCTCTCAGAGAAGTT 642

•

RESULT 9

AR066022

,

LOCUS   AR066022   1999 bp   DNA   PAT   29-SEP-1999
DEFINITION   Sequence 2 from patent US 5849879.
ACCESSION   AR066022
VERSION   AR066022.1 GI:5996238
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 1999)
  AUTHORS   Nguyen,T.D., Polansky,J.R. and Huang,W.
  TITLE   Methods for the diagnosis of glaucoma
  JOURNAL   Patent: US 5849879-A 2 15-DEC-1998;
FEATURES   Location/Qualifiers
     source   1..1999
                     /organism="unknown"
BASE COUNT   537 a   508 c   534 g   420 t
ORIGIN

Query Match   10.4%; Score 640.4; DB 5; Length 1999;
Best Local Similarity   99.8%; Pred. No. 1.2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   5301 agagcttccagaggaggaagcctcaccaagcctctgcaatgaggttcttctgtgcacgttgc 5360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGAGCTTTCCAGAGGAGGAAGCCTCACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60

Qy   5361 tgcagcttgggcctgagatgccagctgccagctgcttctgtctggcctgtctcctgtggtgg 5420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGCAGCTTTGGGCCTGAGATGCCAGCTGCCAGCTGCTTCTGGCCTGTCTCCTGTGGTGG 120

Qy   5421 gatgtggggggccaggacagctcagctcaggagaaggccaatgaccagagtgccgatgccag 5480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGAGAAGGCCAATGACCAGAGTGCCGATGCCAG 180

Qy   5481 tataccttcagtgtggccagtcccaatgaatccagcgtgcccagaagcagcaggccagccatg 5540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCGTGCCCAGAAGCAGCAGGCCAGCCATG 240

Qy   5541 tcagtcatccataacttacagagagacagcagacagcaagacagcacccaaagccttagacctggagggcacc 5600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAGTCATCCATAACTTACAGAGAGACAGCAGACAGCAAGACAGCACCCAAAGCCTTAGACCTGGAGGGCACC 300

Qy   5601 aaagtccgactcagctccctggagagagcctccctccaccacaattgacccttggaccaggctgcc 5660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAAGCTCGACTCAGCTCCCTGGAGAGAGCCTCCCTCCACCACAATTGACCCTTGGACCAGGCTGCC 360

Qy   5661 aggccccaggagagacccaggagggggtgcacaggtggcacccctgaggcggcggggaccgg 5720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGGCCCCAGGAGAGACCCAGGAGGGGGCCACCCTGAGGCGGCGGGGACCGG 420

Qy   5721 gaccagctggaaaacccaaaccagagagagttggagactgctacagacaactcctccgagac 5780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGCTGGAAAACCCAAACCAGAGAGTTGGAGACTGCTACAGACAACTCCTCCGAGAC 480

Qy   5781 aagtcagttctggaggaggaagacgactaaggccaagaaatctggggccagg 5840
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAGTCAGTTCTGGAGGAGGAAGACGACTAAGGCAAGAAAATGAGAATCTGGGGCCAGG 540

Qy   5841 aggttggaaagcagcagcccaggagctggaaggctaaggccagtgtctcccagacc 5900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGGTTGGAAAGCAGCAGCCCAGGAGGTAGCAAGGCTTGAGGAAGGGCCAGTGTCCCAGACC 600

Qy   5901 cgagacactgctcgggctgtgtgccaccaggctctcccagagagaaggt 5942
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CGAGACACTGCTCGGGGCTGTGCCACCAGGCTCTCAGAGAAGTT 642

RESULT 10

AR069089

LOCUS   AR069089   1999 bp   DNA   PAT   29-SEP-1999
DEFINITION   Sequence 2 from patent US 5854415.
ACCESSION   AR069089

VERSION   AR069089.1 GI:6001296
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM Unclassified.
REFERENCE   1 (bases 1 to 1999)
  AUTHORS   Nguyen,T.D., Polansky,J.R. and Huang,W.
  TITLE   Methods for the diagnosis of glaucoma
  JOURNAL   Patent: US 5854415-A 2 29-DEC-1998;
FEATURES   Location/Qualifiers
     source   1.
                     /organism="unknown"
                     1. 1999
BASE COUNT   537 a   508 c   534 g   420 t
ORIGIN

Query Match   10.4%; Score 640.4; DB 5; Length 1999;
Best Local Similarity 99.8%; Pred. No. 1.2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy  5301 agagctttccagaggaagaagcctcaccaagccctgcaatgaggagttgtccagttgc 5360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGAGCTTTCCAGAGGAAGAAGCCTCACCAAGCCCTGCAATGAGGAGTTGTCCAGTTGC 60

Qy  5361 tgcagctttgggcctgagatgtccagtgtctgctgtcttctgtgcctggctgtgtgg 5420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCAGCTTTGGGCCTGAGATGGCCAGTGTGTCCAGCTGCTGTCTTCTGTGCCTGGTGTGG 120

Qy  5421 gatgtggggggccaggacagctcagctcaggaagcccaatgaccagaagtgccgatgccag 5480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGAAGGCCAATGACCAGAGTGCCCGATGCCAG 180

Qy  5481 tatacctttcagttgtggccagtcccaatgaatccagcagcaggacaggacaggccatg 5540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TATACCTTTCAGTTGTGGCCAGTCCCAATGAATCCAGCAGCAGGACAGGAGCAGGCCATG 240

Qy  5541 tcagtcatcaataacttacagagacagcagcaccacccaacccgcctaaacctggaggccacc 5600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAGTCATCAATAACTTACAGAGACAGCAGCACCACCCAACCGTTAGACCTGGAGGCCACC 300

Qy  5601 aaagctcgactcagctcctgagagccctctcctccacaattgaccttggaccaaggctgcc 5660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAAGCTCGACTCAGCTCCTGGAGAGCCCTCTCCTCCACCAATTGACCTTGGACCAGGCTGCC 360

Qy  5661 aggccccaggaggaggggggctgcagggagggggaggtgggggaggtgggggaggacgg 5720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGGCCCCAGGAGACCCCAGGAGGGGGCTGCAGAGGGAGGGGGAGGTGGGGGAGGACGG 420

Qy  5721 gaccagctgaaaccccaaacacaagagagttggagactgcctacacagcaacctcctccagagac 5780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCACCTGGGAAAACCAAAACCAGAGACTTGGAGACTGCCACAACCTCCTCCGAGAC 480

Qy  5781 aagtcagttctggaggaagaagcagcgactaaggcaagaaaaatgagaaactggccagg 5840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAGTCAGTTCTGGAGGAAGAGAAGAGAGCGACTAAGGCAAGAAAAATGAGAAATCTGGCCAGG 540

Qy  5841 aggttggaaagcagcagccaaggaggaggggctaagcggggcccaggtgtccccagacc 5900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGGTTGGAAAGCAGCAGCCAAGGAGGTAGCAAGGCTGAGAAGGGCCCAGTGTCCCCAGACC 600

Qy  5901 cgagacactgctctcggcctgtcccaccaggctcccagagagaaggt 5942
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CGAGACACTGCTCTCGGCGGCTGTCCCACCAGGCTCCCAGAGAAAGTT 642
```

RESULT 11
LOCUS   HSU85257   2000 bp   mRNA   PRI   19-MAR-1998
DEFINITION Human trabecular meshwork inducible glucocorticoid response protein
            (TIGR) mRNA, complete cds.
ACCESSION   U85257
VERSION   U85257.1 GI:2978428
KEYWORDS   .

SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2000)
  AUTHORS   Nguyen,T.D. and Polansky,J.R.
  TITLE   Glucocorticoid effects on HTM cells: Molecular Biology Approaches
  JOURNAL   Glaucoma Update 4, 331-343 (1991)
REFERENCE   2 (bases 1 to 2000)
  AUTHORS   Stone,E.M., Fingert,J.H., Alward,W.L.M., Nguyen,T.D.,
            Polansky,J.R., Sunden,S.L.F., Nishimura,D., Clark,A.F., Nystuen,A.,
            Nichols,B.E., Mackey,D.A., Ritch,R., Kalenak,J.W., Craven,E.R. and
            Sheffield,V.C.
  TITLE   Identification of a gene that causes primary open angle glaucoma
  JOURNAL   Science 275 (5300), 668-670 (1997)
  MEDLINE   97158493
REFERENCE   3 (bases 1 to 2000)
  AUTHORS   Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and
            Polansky,J.R.
  TITLE   Gene structure and properties of TIGR, an olfactomedin-related
            glycoprotein cloned from glucocorticoid-induced trabecular meshwork
            cells
  JOURNAL   J. Biol. Chem. 273 (11), 6341-6350 (1998)
  MEDLINE   98165818
REFERENCE   4 (bases 1 to 2000)
  AUTHORS   Nguyen,T.D. and Polansky,J.R.
  TITLE   Direct Submission
  JOURNAL   Submitted (13-JAN-1997) Ophthalmology, University of California San
            Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
REFERENCE   5 (bases 1 to 2000)
  AUTHORS   Nguyen,T.D.
  TITLE   Direct Submission
  JOURNAL   Submitted (02-APR-1997) Ophthalmology, University of California San
            Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
  REMARK   Sequence update by submitter
REFERENCE   6 (bases 1 to 2000)
  AUTHORS   Nguyen,T.D.
  TITLE   Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Ophthalmology, University of California San
            Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
  REMARK   Sequence update by submitter
COMMENT   On Mar 19, 1998 this sequence version replaced gi:1945067.
FEATURES   Location/Qualifiers
     source   1..2000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_type="primary cultured cells of trabecular meshwork
                     tissue"
                     /chromosome="1"
                     /map="1q23-q24"
     gene   <1..>2000
                     /gene="TIGR"
     5'UTR   <1..37
                     /gene="TIGR"
                     /note="additional 5' UTR sequence deposited as TIGR gene
                     sequence with GenBank Accession Number AF007562"
     CDS   37..1551
                     /gene="TIGR"
                     /codon_start=1
                     /product="trabecular meshwork inducible glucocorticoid
                     response protein"
                     /protein_id="AAC52051.1"
                     /db_xref="GI:1945068"
                     /translation="MRFFCARCCSFGPEMPAVQLLLLACLVWDVGARTAQLRKANDQS
                     GRCQYTFSVASPNESSCPEQSQAMSVIHNLQRDSSTQRLDLEATKARLSSLESLLHQL
                     TLDQAARPQETQDGLQRELGTLRRERDQLETQTRELETAYSNLLRDKSVLEEKKRLR
                     QENENLARRLESSSQEVARLRRGQCPQTRDTARAVPPGSREVSTWNLDTLAFQELKSE
                     LTEVPASRILKESPSGYLRSGEDGTCGGELVWVGEPLTLRTAETITGKYGVWMRDPKP
                     TYPYTQETTWRIDTVGTDVRQVFEYDLISQFMQGYPSKVHILPRPLESTGAVVSGSL
                     YFQGASRTVIRYELNTETVAKEKEIPGAGYHGQFPYSWGGYTDIDLAVDEAGLWVIY
                     STDEAKGAIVLSKLNPENELEQTWETNIRKQSVANAFIICGTLYTVSSYTSADATVN
                     FAYDTGTGISKILTIPFKNRYKYSSMIDYNPLEKKLFAWDNLNMVIYDIKLSKM"
     3'UTR   1552..>2000
```

RESULT 12

```
LOCUS       A84847       2002 bp    DNA            PAT    21-JAN-2000
ACCESSION   A84847
DEFINITION  Sequence 2 from Patent WO9844108.
VERSION     A84847.1  GI:6733711
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2002)
  AUTHORS   Huang,W. and Nguyen,T.D.
  TITLE     DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
  JOURNAL   Patent: WO 9844108-A 08-OCT-1998;
            HUANG WEIDONG (US); NGUYEN THAI D (US)
FEATURES             Location/Qualifiers
     source          1..2002
```

BASE COUNT   538 a   508 c   534 g   420 t
ORIGIN

Query Match   10.4%; Score 640.4; DB 66; Length 2000;
Best Local Similarity 99.8%; Pred. No. 1.2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 5301 agagcttccagaggaggaagcctcaccaagcctctgcaatgagagttcttctgtgcacgttgc 5360
        |||||||| |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    1 AGAGCTTTCCAGAGGAGGAAGCCTCACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60

Qy 5361 tgcagcttgggcctgagatgccagctgctcttcggctgctgggtgtgg 5420
        |||||||| |||||||||||||||||| |||| |||||| |||||||||
Db   61 TGCAGCTTTGGGCCTGAGATGCCAGCTGTTCAGCTGCTTCTTCGGCTGCTGGGTGTGG 120

Qy 5421 gatgtggggccaggacagctcagctcggaaggccaatgaccagagtggccagatgccag 5480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GATGTGGGGCCAGGACAGCTCAGCTCGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180

Qy 5481 tataccttcagtgtggccagtcccaatgaatccagctcagagaagagcagagccaggccatg 5540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTCAGAGAAGAGCAGAGCCAGGCCATG 240

Qy 5541 tcagtcatcccataacttacagagagacgacccaacgcttagacctgggaggccacc 5600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCAGTCATCCATAACTTACAGAGAGACGACCCAACGCTTAGACCTGGGAGGCCACC 300

Qy 5601 aaagctcgactcagctccctgagagagctccctccaccaattgaccttgaccggctgcc 5660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AAAGCTCGACTCAGCTCCCTGGAGAGCTCCTCCACCAATTGACCTTGACCAGGCTGCC 360

Qy 5661 aggccccaggagaaccaggaggagggctggagactggagcccccaggaggagcgg 5720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 AGGCCCCAGGAGGACCAGGAGGAGGGCTGGAGACTGGAGCCCCCAGGAGGAGGCGG 420

Qy 5721 gaccagctggaaacccaaacccagagagttggagactgcctacaggccaacctcctccgagac 5780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GACCAGCTGGAAACCCAAACCCAGAGAGTTGGAGACTGCCTACAGGCCAACCTCCTCCGAGAC 480

Qy 5781 aagtcagttcctggaggagaagaagcaactaaggccaagaaatctggccagg 5840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AAGTCAGTTCTGGAGGAGAAGAAGCAACTAAGGCCAAGAAATGAGAATCTGGCCAG 540

Qy 5841 aggttggaaagcagcagccaggaggtagcaagctgagaagtgtcccagacc 5900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AGGTTGGAAAGCAGCAGCCAGGAGGTAGCAAGCTGAGAAGTGTCCCAGACC 600

Qy 5901 cgagacactgctcgggcttgtgtgtgccaccaggcctccagagaaggt 5942
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 CGAGACACTGCTCGGGCTTGTGTGTGCCACCAGGCCTCCAGAGAAGTT 642
```

RESULT 13

```
LOCUS       A84850       2000 bp    DNA            PAT    21-JAN-2000
ACCESSION   A84850
DEFINITION  Sequence 2 from Patent WO9844107.
VERSION     A84850.1  GI:6733713
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2000)
  AUTHORS   Huang,W. and Nguyen,T.D.
  TITLE     DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
  JOURNAL   Patent: WO 9844107-A 08-OCT-1998;
            UNIVERSITY OF CALIFORNIA (US); HUANG WEIDONG (US)
FEATURES             Location/Qualifiers
     source          1..2000
                     /organism="unidentified"
                     /db_xref="taxon:32644"
                     /organism="unidentified"
```

BASE COUNT   538 a   508 c   535 g   421 t
ORIGIN

Query Match   10.4%; Score 640.4; DB 5; Length 2002;
Best Local Similarity 99.8%; Pred. No. 1.2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 5301 agagcttccagaggaggaagcctcaccaagcctctgcaatgagagttcttctgtgcacgttgc 5360
        |||||||| |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    1 AGAGCTTTCCAGAGGAGGAAGCCTCACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60

Qy 5361 tgcagcttgggcctgagatgccagctgctcttcggctgctgggtgtgg 5420
        |||||||| |||||||||||||||||| |||| |||||| |||||||||
Db   61 TGCAGCTTTGGGCCTGAGATGCCAGCTGTTCAGCTGCTTCTTCGGCTGCTGGGTGTGG 120

Qy 5421 gatgtggggccaggacagctcagctcggaaggccaatgaccagagtggccagatgccag 5480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GATGTGGGGCCAGGACAGCTCAGCTCGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180

Qy 5481 tataccttcagtgtggccagtcccaatgaatccagctcagagaagagcagagccaggccatg 5540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTCAGAGAAGAGCAGAGCCAGGCCATG 240

Qy 5541 tcagtcatcccataacttacagagagacgacccaacgcttagacctgggaggccacc 5600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCAGTCATCCATAACTTACAGAGAGACGACCCAACGCTTAGACCTGGGAGGCCACC 300

Qy 5601 aaagctcgactcagctccctgagagagctccctccaccaattgaccttgaccaggctgcc 5660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AAAGCTCGACTCAGCTCCCTGGAGAGCTCCTCCACCAATTGACCTTGACCAGGCTGCC 360

Qy 5661 aggccccaggagaaccaggaggagggctggagactggagcccccaggaggagcgg 5720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 AGGCCCCAGGAGGACCAGGAGGAGGGCTGGAGACTGGAGCCCCCAGGAGGAGGCGG 420

Qy 5721 gaccagctggaaacccaaacccagagagttggagactgcctacaggccaacctcctccgagac 5780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GACCAGCTGGAAACCCAAACCCAGAGAGTTGGAGACTGCCTACAGGCCAACCTCCTCCGAGAC 480

Qy 5781 aagtcagttcctggaggagaagaagcaactaaggccaagaaatctggccagg 5840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AAGTCAGTTCTGGAGGAGAAGAAGCAACTAAGGCCAAGAAATGAGAATCTGGCCAG 540

Qy 5841 aggttggaaagcagcagccaggaggtagcaagctgagaagtgtcccagacc 5900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AGGTTGGAAAGCAGCAGCCAGGAGGTAGCAAGCTGAGAAGTGTCCCAGACC 600

Qy 5901 cgagacactgctcgggcttgtgtgtgccaccaggcctccagagaaggt 5942
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 CGAGACACTGCTCGGGCTTGTGTGTGCCACCAGGCCTCCAGAGAAGTT 642
```

```
BASE COUNT        538 a      506 c      534 g      422 t
ORIGIN          /db_xref="taxon:32644"

Query Match
Best Local Similarity    10.3%;
Matches  638;  Conservative   0;  Pred. No. 1.4e-128;   Mismatches   4;   Indels   0;   Gaps   0;
                         Score 635.6;  DB 5;    Length 2000;

Qy   5301 agagctttccagaggaaagccctcaccaagccctgcaatgagctgaggttgttcttctgtgtcacgttgc 5360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGAGCTTTCCAGAGGAAAGCCCTCACCAAGCCCTGCAATGAGGTTGTTCTTCTGTGTCACGTTGC 60

Qy   5361 tgcagctttgggcctgagagatgccaagctgtcctgctctgctggttgtgtg 5420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCAGCTTTGGGCCTGAGAGATGCCAGTGCCAGCTGTCTTCCAGCTGCTGTCTGGCCTGGGTGTGG 120

Qy   5421 gatgtggggggccaggacagctcagctcaggaggaagtggccgatgccag 5480
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GATGTGGGGGGCCAGGACAGCTCAGGAGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180

Qy   5481 tatacttcagttgtggtgccagtcccaatgaatccacgctgtgcccgagagc 5540
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TATACTTCAGTTGTGGTGCCCAGTCCCAATGAATCCACGCTGTGCTGGGCTGGGGTGTGG 240

Qy   5541 tcagtcatccataactttacagaggacagcagcagaacgcttagacctggag 5600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCAGTCATCCATAACTTTACAGAGGACAGCAGCAGAACGCTTAGACCTGGAGGCCACC 300

Qy   5601 aaagctcgactctggaggagagctcctcccaccaattgaccttggac 5660
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAAGCTCGACTCTGGAGGAGAGCTCCTCCCACCAATTGACCTTGGACACAGGCTTCC 360

Qy   5661 aggcccaggagagaccccaggagggggctgcagaggggggccgg 5720
          ||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGCCCAGGAGACCCCAGGAGGGGGCTGCAGAGGGGGCCGG 420

Qy   5721 gaccagctggaaacccaaaccagagagttggggagactg 5780
          |||||||||||||||||||||||||||||||||||||||
Db    421 GACCAGCTGGAAACCCAAACCAGAGTTGGAGACTGCCTCAGCACACCTCCTCCGAGAC 480

Qy   5781 aagtcagttctggggaggaagga 5840
          |||||||||||||||||||||||
Db    481 AAGTCAGTTCTGGGAGGAAGGAGGAGAAGGCCACTAAGGCAAGAAAATGAGAAATCTGGCCCAG 540

Qy   5841 aggttggaaagcagcagcgcacagagcacccaagtt 5900
          ||||||||||||||||||||||||||||||||||||
Db    541 AGGTTGGAAAGCAGCAGCGCACAGAGGGGGCCCAGTGTCCCAGTACC 600

Qy   5901 cgagaacaactgctccgggcgtgcccacccaggagaagaggt 5942
          ||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAGACACTGCTCCGGGCGTGCCCACCCAGCAGGAAGTT 642
```

```
BASE COUNT        570 a      517 c      537 g      437 t
ORIGIN

Query Match
Best Local Similarity    10.2%;                Score 626.4;  DB 66;    Length 2061;
Matches  627;  Conservative   0;  Pred. No. 1.4e-126;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   5315 gaagcctcaccaagccctgcaatgagctgaggttgttcttctgtgtcacgttgctcaagctttgggcc 5374
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAAGCCTCACCAAGCCCTGCAATGAGGTTCTTCTGTGTCACGTTGCTCAAGCTTTGGGCC 60

Qy   5375 tgagatgccaagctgtccagctgctgtcttctggcctggtcgtggggggccag 5434
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGAGATGCCAGCTGTCCAGCTGCTGTCTTCTGGCCTGGTCGTGGGGGGCCAG 120

Qy   5435 gacagctcagctcaggaggaagagccaatgaccagagtggccgatgccagtataaccttcagtgt 5494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACAGCTCAGCTCAGGAAGGCCAATGACCAGAGTGGCCGATGCCAGTATAACCTTCAGTGT 180

Qy   5495 ggccagtcccaatgaatccacgctgccccagagccgagagcaggcagccagtcagtcatccataa 5554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGCCAGTCCCAATGAATCCACGCTCCCAGAGCAGGCAGCCAGTCAGTCATCCATAA 240

Qy   5555 cttacagaggagacagcagcagcacccaacgcttagacctggaggccaccaaagctcgactcag 5614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTTACAGAGGAGACAGCAGCAGCACCCAAACGCTTAGACCTGGAGGCCACCAAAGCTCGACTCAG 300
```

```
RESULT 15

LOCUS       A84848      1512 bp    DNA                  PAT     21-JAN-2000
DEFINITION  Sequence 3 from Patent WO9844108.
ACCESSION   A84848
VERSION     A84848
            A84848.1  GI:6733712
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1512)
  AUTHORS   Huang,W. and Nguyen,T.D.
  TITLE     DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
  JOURNAL   Patent: WO 9844108-A 08-OCT-1998;
            HUANG WEIDONG (US); NGUYEN THAI D (US)
FEATURES             Location/Qualifiers
     source          1..1512
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      392 a    406 c    423 g    291 t
ORIGIN
```

```
Query Match         9.8%;  Score 604.4;  DB 5;  Length 1512;
Best Local Similarity   99.8%;
Matches  605;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       5337 atgaggttctctgtcacgtgtctgcagcttggggcctggagtagccagctgtccagctg 5396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGGTTCTCTGTCACGTGTCTGCAGCTTGGGCCTGGAGTAGCCAGCTGTCCAGCTG 60

Qy       5397 ctgcttctcggcctgcctggtgtgggatggtggggccagaacagctccagcgaaggcc 5456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGCTTCTCGGCCTGCCTGGTGTGGGATGGTGGGGCCAGAGCAGCTTCAGGGAAGGCC 120

Qy       5457 aatgaccaccagagtggccgatcccagtatacccttcagtgtggcccagtcccaatgaatccagc 5516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATGACCACCAGAGTGGCCGATCCCAGTATACCTTCAGTGTGGCCCAGTCCCAATGAATCCAGC 180

Qy       5517 tgcccagagcagcaggccaagtcagtcaatccatacttacagagagagacacagcacc 5576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCCAGAGCAGCAGGCCAGGCCATGTCAGTCAGTCAATAACTTACAGAGAGACAGCACC 240

Qy       5577 caacgcttagacctggagaggccacacaaagtccgactcccttggagagacctctccac 5636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAACGCTTAGACCTGGAGAGGCCACACAAAGTCCGACTCCCTCCTGGAGAGGCTCCTCCAC 300

Qy       5637 caatgaccttggacaggcgtgctgcaggctgcagctgagggggacccagggggagggggag 5696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAATTGACCTTGGACCTGGAGAGATGGCAGGCTGCTGCAGGCTGCAGCTGGGGCTGCAGAGGGGAG 360

Qy       5697 ctgggccaccctgagtcgaggcgggagaccagcctggaaatccaaacccaagagagtttgggact 5756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGGCACCCTGAGTCGGGGAGCGGGGAGACCAGCCCAAACCCAAAACCAGAGAGTTGGAGACT 420

Qy       5757 gcctacagccaacctcctccgagacaagtcagttctggaggaaggaagagaagacggaactaagg 5816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCTACAGCCAACCTCCTCCGAGACAAGTCAGTTCTGGAGGAAGGAAGAGAAGCGGACTAAGG 480

Qy       5817 caagaaaatgagaatctggtccaggggtttggaaagcagcagcgaggaggtaggcaaggctg 5876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAGAAAATGAGAAATCTGGCCCAGGAGGTTGGAAAGCAGCAGCCAAGGCTG 540

Qy       5877 agaagggccagtgtgtcccagaccgagacactgctcggggctgtgccacaggyctccaga 5936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAAGGGGCCAGTGTGTCCCCAGACCCCAGGAGACACTGCTCGGGGCTGTGCCACCAGGGCTCCAGA 600

Qy       5937 gaaggt 5942
              ||||||
Db        601 GAAGTT 606

Search completed: December  3, 2000, 18:35:10
Job time: 43924 sec
```

(Right column, separate alignment)

```
Qy       5615 ctccctgggagagcctcctccaccaattgacctggaccaggcgtgccaggcccccaggagac 5674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCCTGGACAGGCCTCCTCCTCCAATTGACCTTGGACCTTGACCTTGCCAGGCCTGCCAGGGAGAC 360

Qy       5675 ccaggagggggctgcagaggcgggagcggggagaccagccagctggaaac 5734
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGGAGGGGGCTGCAGAGGGGAGCTGGGCACCCTGAGGGGCGGGGAGCCGGGGAAAC 420

Qy       5735 ccaaaccaagagagtgtgggaagactgcctcacagacaacaagtcagttctgga 5794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCAAAACCAGAGAGTTGGAGACTGCCTACAGCCAACCTCCTCCGAGACAAGTCAGTTCTGGA 480

Qy       5795 ggaagaagaggaaggcgactaaggcaagaaaatgagaatctgcaggcagaaagcag 5854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGAAGGAAGAGAAGCGGACTAAGGCAAGAAAATGAGAAATCTGGCCCAGGAGGTTGGAAAGCAG 540

Qy       5855 cagcgaggaggtaggcaaggctgagaaggggccagtgtgtcccccagaccgagacactgctcg 5914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGCCAAGGCTGAGAAGGGGCCAGTGTGTCCCCAGACCCCAGGAGACACTGCTCG 600

Qy       5915 ggctgtgccaccaggctccagagagaaggt 5942
              ||||||||||||||||||||||||||||
Db        601 GGCTGTGCCACCAGGCTCCAGAGAAGTT 628
```